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(54) **METHODS AND MATERIALS FOR CANINE BREED IDENTIFICATION**

(75) Inventors: **Elaine Ostrander**, Seattle, WA (US); **Leonid Kruglyak**, Seattle, WA (US); **Heidi G Parker**, Seattle, WA (US); **Lisa V Kim**, Sammamish, WA (US); **Matthew Stephens**, Seattle, WA (US); **Tiffany B Malek**, Seattle, WA (US); **Nathan B Sutter**, Seattle, WA (US); **Scott Carlson**, Seattle, WA (US)

(73) Assignee: **Fred Hutchinson Cancer Research Center**, Seattle, WA (US)

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(58) **Field of Classification Search** .... None
See application file for complete search history.

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Primary Examiner—Mary K Zeman
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(57) **ABSTRACT**

In one aspect, the invention provides methods for determining the contributions of canid populations to a canid genome. The methods comprise the steps of: (a) obtaining the identity of one or both alleles in a test canid genome for each of a set of markers; and (b) determining the contributions of canid populations to the test canid genome by comparing the alleles in the test canid genome to a database comprising canid population profiles, wherein each canid population profile comprises genotype information for the set of markers in the canid populations.

44 Claims, 2 Drawing Sheets

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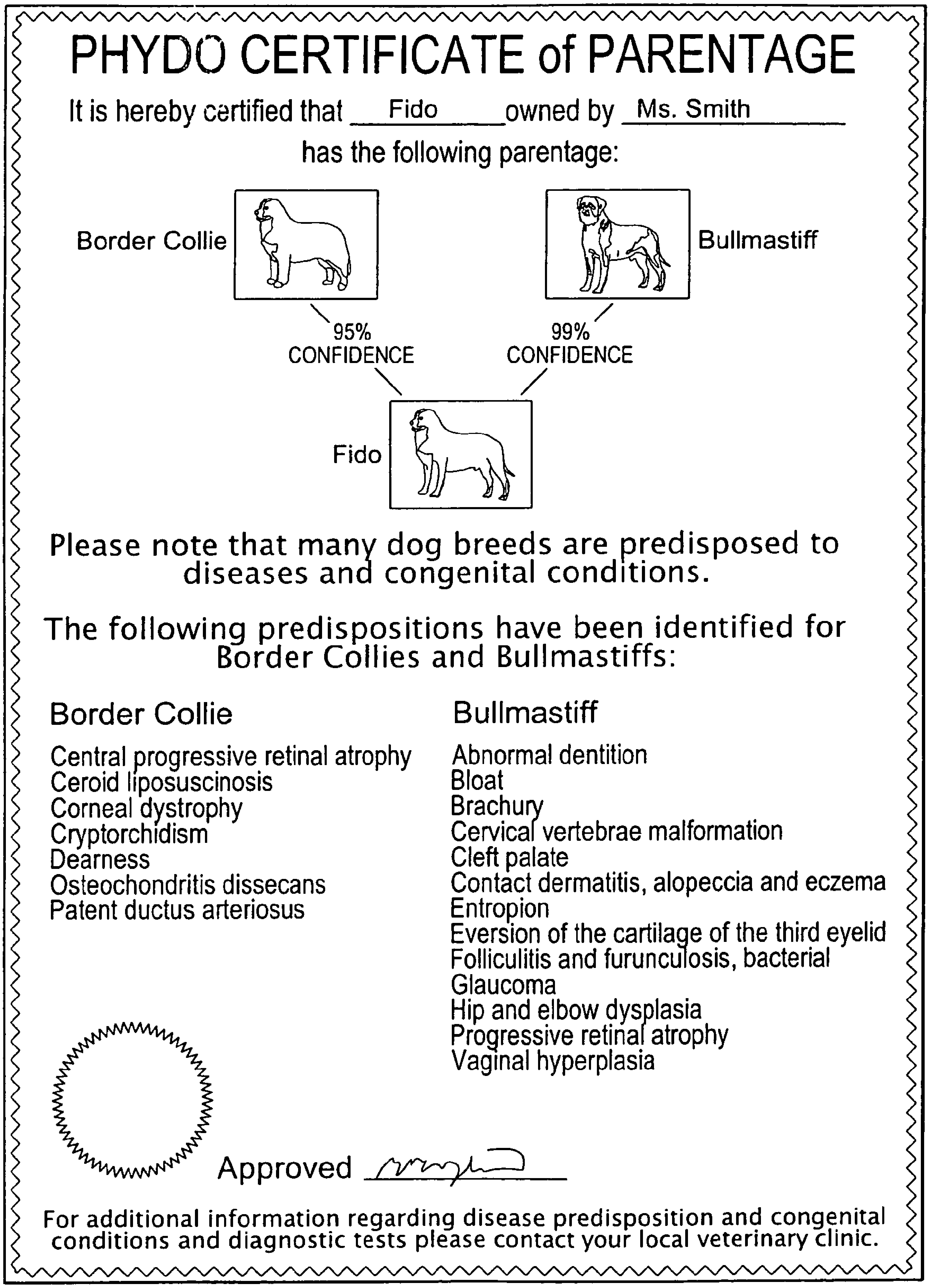

PHYDO CERTIFICATE of PARENTAGE

It is hereby certified that Fido owned by Ms. Smith
has the following parentage:

Border Collie

Bullmastiff

95% CONFIDENCE

99% CONFIDENCE

Fido

Please note that many dog breeds are predisposed to diseases and congenital conditions.

The following predispositions have been identified for Border Collies and Bullmastiffs:

Border Collie	Bullmastiff
Central progressive retinal atrophy Ceroid liposuscinosis Corneal dystrophy Cryptorchidism Dearness Osteochondritis dissecans Patent ductus arteriosus	Abnormal dentition Bloat Brachury Cervical vertebrae malformation Cleft palate Contact dermatitis, alopeccia and eczema Entropion Eversion of the cartilage of the third eyelid Folliculitis and furunculosis, bacterial Glaucoma Hip and elbow dysplasia Progressive retinal atrophy Vaginal hyperplasia

Approved

For additional information regarding disease predisposition and congenital conditions and diagnostic tests please contact your local veterinary clinic.

Fig.1.

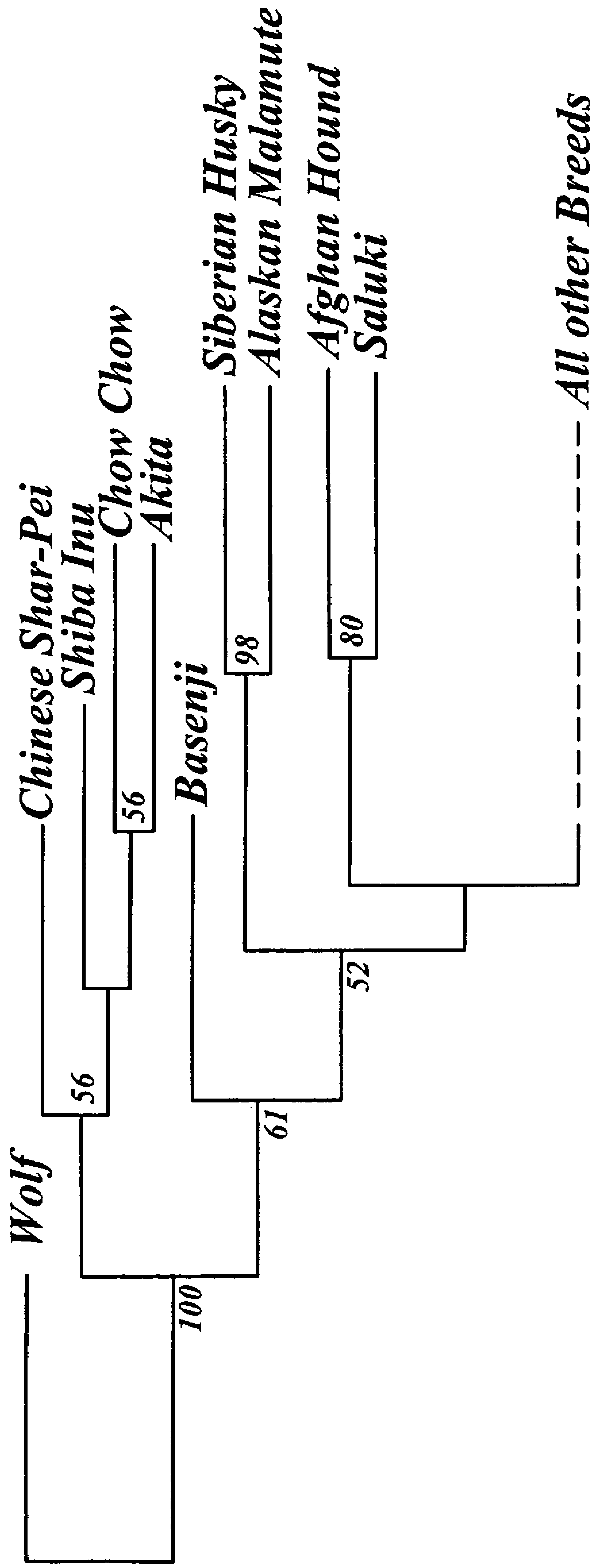
Wolf
Chinese Shar-Pei
Shiba Inu
Chow Chow
Akita
Basenji
Siberian Husky
Alaskan Malamute
Afghan Hound
Saluki
All other Breeds
100
56
56
61
52
98
80

Fig.2.

METHODS AND MATERIALS FOR CANINE BREED IDENTIFICATION

CROSS-REFERENCE TO RELATED APPLICATION

This application claims the benefit of U.S. Provisional Application No. 60/530,464, filed Dec. 17, 2003.

STATEMENT OF GOVERNMENT LICENSE RIGHTS

This invention was made with government support under HG300035 awarded by National Institutes of Health. The government has certain rights in the invention.

FIELD OF THE INVENTION

The invention relates to determining the contribution of one or more canid populations to the genome of a canid using polymorphic markers.

BACKGROUND OF THE INVENTION

Canis familiaris, the domestic dog, is a single species divided into more than 400 phenotypically divergent genetic isolates termed breeds, 152 of which are recognized by the American Kennel Club in the United States (American Kennel Club (1998) *The Complete Dog Book*, eds. Crowley & Adelman, Howell Book Hues, New York, N.Y.). Distinct breeds of dog are characterized by unique constellations of morphology, behavior, and disease susceptibility (Ostrander et al. (2000) *Trends in Genetics* 16:117-23). A variety of dog morphologies have existed for millennia, and reproductive isolation between them was formalized with the advent of breed clubs and breed standards in the mid 19th century. Since that time, the promulgation of the "breed barrier" rule—no dog may become a registered member of a breed unless both its dam and sire are registered members—has ensured a relatively closed genetic pool among dogs of each breed.

Over 350 inherited disorders segregate in the purebred dog population (Patterson et al. (1988) *J. Am. Vet. Med. Assoc.* 193:1131.) Many of these mimic common human disorders and are restricted to particular breeds or groups of breeds as a result of aggressive inbreeding programs used to generate specific morphologies.

There are many potential uses for objectively determining the breed of an individual dog, such as the certification of dogs as belonging to a particular breed. Because historical records vary in reliability from breed to breed, a genetic analysis that does not rely on prior population information is the most direct and accurate method for determining population structure. Over the past decade, molecular methods have been used to enhance our understanding of wild canid species and to determine their relationships to the domestic dog. Mitochondrial DNA sequence analyses describe the relationship between the domestic dog and the wolf, elucidating the multiple domestication events that occurred 40,000-100,000 years ago (Vila et al. (1997) *Science* 276:1687-9; Savolainen et al. (2002) *Science* 298:1610-3, Leonard et al. (2002) *Science* 298:1613-6). However, the evolution of mitochondrial DNA is too slow to allow inference of relationships among modern dog breeds, most of which have existed for fewer than 400 years. In addition, phylogenetic distances measures and tree building programs are not equipped to deal with reticulate evolution as is commonly observed in dog populations (Zajc et al. (1997) *Mamm. Genome* 8(3):182-5; Koskinen & Bredbacka (2000) *Animal Genetics* 31:310-17; Irion et al. (2003) *J. Hered.* 94(1):81-7). One previous study showed that nuclear microsatellite loci could be used to assign dogs from five breeds to their breed of origin, demonstrating large genetic distances among these breeds (Koskinen (2003) *Anim. Genet.* 34:297). Another study used microsatellites to detect relatedness of two breed pairs in a collection of 28 breeds but could not establish broader phylogenetic relationships among the breeds (Irion et al. (2003) *J. Hered* 94:81-7). The failure to find such relationships could reflect the properties of microsatellite loci (Irion et al. (2003) *J. Hered.* 94:81-7), the limited number of breeds examined, or the analytical methods used in the study. Alternatively, it may reflect the complex structure in purebred dog populations, due to the recent origin of most breeds and the mixing of ancestral types in their creation.

There is a need for methods for defining related groups of breeds and for unambiguously identifying breed contributions to the genome of an individual dog. The present invention addresses this and other needs.

SUMMARY OF THE INVENTION

In one aspect, the invention provides methods for determining the contributions of canid populations to a canid genome. The methods comprise the steps of: (a) obtaining the identity of one or both alleles in a test canid genome for each of a set of markers; and (b) determining the contributions of canid populations to the test canid genome by comparing the alleles in the test canid genome to a database comprising canid population profiles, wherein each canid population profile comprises genotype information for the set of markers in the canid population. The set of markers may comprise at least about five markers, for example, at least about five markers set forth on the map of the canine genome. Exemplary markers suitable for use in the methods of the invention include, for example, microsatellite markers, single nucleotide polymorphisms (SNPs), mitochondrial markers, and restriction fragment length polymorphisms. For example, the set of markers may comprise at least 5 of the SNP markers set forth in Table 2, and/or at least 5 microsatellite markers set forth in Table 1. The set of markers may comprise one or more population-specific markers, such as one or more population-specific SNP markers or one ore more population-specific microsatellite markers. For example, one or more SNP markers may be selected from the group consisting of 372c5t-82, 372e13t-57, 372m6t-88, 372m23t-76, 373a15t-112, 373e1t-50, 373e1t-130, 373g19t-246, 373i8s-224, 373k8s-181, 372c5s-168, 372C15S-196, 372e15s-71, and 373a21t-93.

The identity of one or both alleles in a test canid genome for each of the set of markers may be obtained using methods standard in the art, such as hybridization, Polymerase Chain Reaction, size fractionation, DNA sequencing, etc. For example, step (a) of the methods may comprise amplifying genomic DNA of the test canid using primers specific for each of the set markers and determining the size of the amplification product. Step (a) may also comprise amplifying genomic DNA of the test canid using primers specific for each of the set of markers and determining the nucleotide sequence of the amplification product. In some embodiments, the primers are selected from the group consisting of SEQ ID NOs:1-200. In some embodiments, the primers are selected from the group consisting of SEQ ID NOs:1-244-327.

The genotype information in a canid population profile may comprise information such as the identity of one or both alleles of most or all the markers in the set of markers in one or more canids that are members of that canid population, and/or estimated allele frequencies for at least one allele of most or all of the markers in the set of markers in that canid population. Each estimated allele frequency in a canid population profile is typically based on the identities of one or both alleles in at least two genomes of canids that are members of the canid population. The database of canid population profiles may comprise between about five and several hundreds of canid population profiles, such as at least about 100 canid population profiles. In some embodiments, the canid population profiles comprise profiles of registered breeds, such as breeds registered by the American Kennel Club.

In some embodiments, the set of markers comprises fewer than about 1500 SNP markers and wherein the method determines the contributions of at least 87 canid populations to the test canid genome. In some embodiments, the set of markers comprises fewer than about 200 SNP markers (such as about 100 SNP markers, or about 50 SNP markers) and wherein the method determines the contributions of at least 87 canid populations to the test canid genome.

In step (b) of the method, the likelihood that one or more canid populations contributed to the test canid genome may be determined using any suitable algorithm, such as Bayesian model-based clustering algorithms or assignment algorithms. In some embodiments, step (b) comprises determining the probability that a specific canid population contributed to the genome of the test canid by determining the conditional probability that the alleles in the test canid genome would occur in the specific canid population divided by the sum of conditional probabilities that the alleles in the test canid genome would occur in each canid population in the database. In some embodiments, step (b) comprises discriminating between the contributions of two or more genetically related canid populations to the test canid genome by comparing the alleles in the test canid genome to a database comprising profiles of the two or more genetically related canid populations. Exemplary genetically related canid populations include, but are not limited to, Belgian Sheep Dog and Belgian Tervuren; Collie and Shetland Sheep Dog; Whippet and Greyhound; Siberian Husky and Alaskan Malamute; Mastiff and Bullmastiff; Greater Swiss Mountain Dog and Bernese Mountain Dog; West Highland White Terrier and Cairn Terrier; and Lhasa Apso, Shih Tzu, and Pekinese.

In some embodiments, the methods of the invention further comprise the step of providing a document displaying the contributions of one or more canid populations to the genome of the test canid genome. The document may provide information regarding the one or more canid populations that contributed to the genome of the test canid or the test canid, such as health-related information (e.g., disease predispositions), insurance information, or any other kind of information. The document may also provide a certification of the contributions of one or more canid populations to the genome of the test canid genome. In some embodiments, the document provides a representation (e.g., a photograph, drawing, or other depiction) of the one or more canid populations that contributed to the genome of the test canid.

In some embodiments, the invention provides methods for defining one or more canid populations, comprising: (a) for each of a set of canid genomes, obtaining the identity of one or both alleles for each of a set of markers; and (b) defining one or more canid populations by determining the likelihood that one or more members of the set of canid genomes define distinct canid populations characterized by a set of allele frequencies for each marker using statistical modeling.

In another aspect, the invention provides substrates comprising nucleic acid sequences for obtaining the identity of one or both alleles in a canid genome for each of a set of markers.

In a further aspect, the invention provides a computer-readable medium comprising a data structure stored thereon for use in distinguishing canid populations, the data structure comprising: (a) a marker field, which is capable of storing the name of a marker or of an allele of the marker; and (b) a genotype information field, which is capable of storing genotype information for the marker in a canid population, wherein a record comprises an instantiation of the marker field and an instantiation of the genotype information field and a set of records represents a canid population profile. For example, the genotype information field may be capable of storing an estimate of the frequency of the allele of a marker (e.g., an SNP marker) in a canid population. The genotype information field may also be capable of storing the identity of one or both alleles of each of a set of markers in one or more canids that are members of that canid population. In some embodiments, the computer readable medium comprises a substrate having stored thereon: computer-readable information comprising (a) a data structure for use in distinguishing canid populations, the data structure comprising: (i) a marker field, which is capable of storing the name of a marker or of an allele of the marker; and (ii) a genotype information field, which is capable of storing genotype information for the marker in a canid population, wherein a record comprises an instantiation of the marker field and an instantiation of the genotype information field and a set of records represents a canid population profile; and, (b) computer-executable instructions for implementing a method for determining the contributions of canid populations to a canid genome, comprising: (i) obtaining the identity of one or both alleles in a test canid genome for each of a set of markers; and (ii) determining the contributions of canid populations to the test canid genome by comparing the alleles in the test canid genome to a database comprising canid population profiles, wherein each canid population profile comprises genotype information for the set of markers in the canid population.

BRIEF DESCRIPTION OF THE DRAWINGS

The foregoing aspects and many of the attendant advantages of this invention will become more readily appreciated as the same become better understood by reference to the following detailed description, when taken in conjunction with the accompanying drawings, wherein:

FIG. **1** shows an exemplary document displaying the contributions of two canid populations (Border Collie and Bullmastiff) to the genome of a test canid (Fido), along with information about disease predispositions for the two canid populations.

FIG. **2** shows a consensus neighbor-joining tree of 85 dog breeds and the gray wolf, as described in EXAMPLE 4. Nine breeds that form branches with statistical support are shown. The remaining 76 breeds show little phylogenetic structure and have been combined into one branch labeled "All Other Breeds" for simplification. The trees that formed the consensus are based on the chord distance measure. 500 bootstrap replicates of the data were carried out, and the fraction of bootstraps supporting each branch is indicated at the corresponding node as a percentage for those branches supported in over 50% of the replicates. The wolf population at the root of the tree consists of 8 individuals, one from each of the following countries: China, Oman, Iran, Sweden, Italy, Mexico, Canada and the United States. Branch lengths are proportional to bootstrap values.

DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENT

The specification hereby incorporates by reference in their entirety the files contained on the two compact discs filed herewith. The first compact disc includes Tables 3 and 4, the second compact disc includes a sequence listing.

Unless specifically defined herein, all terms used herein have the same meaning as they would to one skilled in the art of the present invention.

In a first aspect, the invention provides methods for determining the contributions of canid populations to a canid genome, comprising: (a) obtaining the identity of one or both alleles in a test canid genome for each of a set of markers; and (b) determining the contributions of canid populations to the test canid genome by comparing the alleles in the test canid genome to a database comprising canid population profiles, wherein each canid population profile comprises genotype information for the set of markers in the canid population.

As used here, the term "determining the contributions of canid populations" refers to estimating or inferring using statistical methods the contributions of canid populations to draw conclusions regarding whether one or more canid populations contributed to the genome of a test canid.

The term "canid" as used herein refers to an animal that is a member of the family Canidae, which includes wolves, jackals, foxes, coyote, and the domestic dog. For example, a canid may be a domestic dog, a wolf, or an animal that has some genetic contributions from more than one species of the family Canidae. The term "canid population" refers to a group of canids related by descent, such as a domestic dog breed. The term "breed" refers to an intraspecies group of animals with relatively uniform phenotypic traits that have been selected for under controlled conditions by man. For example, the American Kennel Club (AKC) recognizes 152 breeds distributed in seven breed groups (Herding, Hound, Nonsporting, Sporting, Terrier, Toy, and Working) (American Kennel Club (1998) *The Complete Dog Book*, eds. Crowley & Adelman, Howell Book Hues, New York, N.Y.). The methods of the invention may be used to estimate the genetic contributions of any dog breed, including, but not limited to Afghan Hound, Airedale Terrier, Akita, Alaskan Malamute, American Eskimo Dog, American Foxhound, American Hairless Rat Terrier, American Staffordshire Terrier, American Water Spaniel, Australian Cattle Dog, Australian Shepherd, Australian Terrier, Basenji, Basset Hound, Beagle, Bearded Collie, Bedlington Terrier, Belgian Laekenois, Belgian Malinois, Belgian Sheepdog, Belgian Tervuren, Bernese Mountain Dog, Bichon Frise, Bloodhound, Border Collie, Border Terrier, Borzoi, Boston Terrier, Bouvier des Flandres, Boykin Spaniel, Boxer, Briard, Brittany, Bulldog, Brussels Griffon, Bullmastiff, Bull Terrier, Cairn Terrier, Cardigan Welsh Corgi, Cavalier King Charles Spaniel, Chesapeake Bay Retriever, Chihuahua, Chinese Crested, Chinese Shar-Pei, Chow Chow, Clumber Spaniel, Cocker Spaniel, Collie, Curly-Coated Retriever, Dachshund, Dalmatian, Dandie Dinmont Terrier, Doberman Pinscher, Dogo Canario, English Cocker Spaniel, English Foxhound, English Setter, English Springer Spaniel, Entlebucher Mountain Dog, Field Spaniel, Flat-Coated Retriever, French Bulldog, German Longhaired Pointer, German Shepherd Dog, German Shorthaired Pointer, German Wirehaired Pointer, Giant Schnauzer, Golden Retriever, Gordon Setter, Great Dane, Great Pyrenees, Greater Swiss Mountain Dog, Greyhound, Harrier, Havanese, Ibizan Hound, Irish Setter, Irish Terrier, Irish Water Spaniel, Irish Wolfhound, Italian Greyhound, Jack Russell Terrier, Keeshond, Kerry Blue Terrier, Komondor, Kuvasz, Labrador Retriever, Leonberger, Lhasa Apso, Lowchen, Maltese, Manchester Terrier—Standard, Manchester Terrier—Toy, Mastiff, Miniature Bull Terrier, Miniature Pinscher, Miniature Poodle, Miniature Schnauzer, Munsterlander, Neapolitan Mastiff, Newfoundland, New Guinea Singing Dog, Norwegian Elkhound, Norwich Terrier, Old English Sheepdog, Papillon, Pekingese, Pembroke Welsh Corgi, Petit Basset Griffon Vendeen, Pharaoh Hound, Pointer, Polish Lowland Sheepdog, Pomeranian, Portuguese Water Dog, Presa Canario, Pug, Puli, Pumi, Rhodesian Ridgeback, Rottweiler, Saint Bernard, Saluki, Samoyed, Schipperke, Scottish Deerhound, Scottish Terrier, Silky Terrier, Shetland Sheepdog, Shiba Inu, Shih Tzu, Siberian Husky, Smooth Fox Terrier, Soft Coated Wheaten Terrier, Spinone Italiano, Staffordshire Bull Terrier, Standard Poodle, Standard Schnauzer, Sussex Spaniel, Tibetan Spaniel, Tibetan Terrier, Toy Fox Terrier, Toy Poodle, Vizsla, Weimaraner, Welsh Springer Spaniel, Welsh Terrier, West Highland White Terrier, Wirehaired Pointing Griffon, Whippet, Yorkshire Terrier.

The methods of the invention may also be used to determine genetic contributions from canid populations that are subsets of recognized breeds, for example, a group of Dalmatians originating from a particular breeder, or a group of canids that are not, or not yet, recognized as a breed. Similarly, the methods of the invention may be used to determine genetic contributions from canid populations that are not domestic dogs.

The first step in the methods of the invention comprises obtaining the identity of one or both alleles in a test canid genome for each of a set of markers. The term "marker" refers to any polymorphic genomic locus that is sufficiently informative across the canid populations used in the methods of the invention to be useful for estimating the genetic contribution of these canid populations to the genome of a test canid. A genomic locus is polymorphic if it has at least two alleles. The term "allele" refers to a particular form of a genomic locus that may be distinguished from other forms of the genomic locus by its nucleic acid sequence. Thus, different alleles of a genomic locus represent alternative nucleic acid sequences at that locus. In any individual canid genome, there are two alleles for each marker. If both alleles are the same, the genome is homozygous for that marker. Conversely, if the two alleles differ, the genome is heterozygous for that marker.

Population-specific alleles are alleles that are present at some frequency in one canid population but have not been observed in the sampled canids from comparison canid populations (although they may be present at a significantly lower frequency). Population-specific alleles may be used to assign an individual to a particular population. Accordingly, the difference in allele frequencies between populations can be used for determining genetic contributions.

A "set of markers" refers to a minimum number of markers that are sufficient for determining the genetic contribution of the canid populations used in the methods of the invention to the genome of a test canid. The minimum number of markers required depends on the informativeness of the markers for the particular canid populations that are being used, as further described below. The set of markers may comprise at least about 5 markers, at least about 10 markers, at least about 50 markers, or more than about 100 markers.

Representative markers that may be used according to the invention include microsatellite markers, mitochondrial markers, restriction fragment length polymorphisms, and single nucleotide polymorphisms (SNPs). Useful canine microsatellite markers include, but are not limited to, dinucleotide repeats, such as $(CA)_n$, trinucleotide repeats, and tetranucleotide repeats, such as $(GAAA)_n$ (Francisco et al. (1996) *Mamm. Genome* 7:359-62; Ostrander et al. (1993) *Genomics* 16:207-13). Exemplary markers for use in the methods of the invention include the microsatellite markers set forth in Table 1, the SNP markers set forth in Table 2, and the markers described in Guyon et al. (2003) *Proc. Natl. Acad. Sci U.S.A.* 100(9):5296-5301. The set of markers used in the methods of the invention may comprise at least about 5 markers from the microsatellite markers in Table 1 and/or at least about 5 markers from the SNP markers in Table 2. In some embodiments, the set of markers are selected from the group consisting of 372c5t-82, 372e13t-57, 372m6t-88, 372m23t-76, 373a15t-112, 373e1t-50, 373e1t-130, 373g19t-246, 373i8s-224, 373k8s-181, 372c5s-168, 372C15S-196, 372e15s-71, and 373a21t-93. In some embodiments, a set of markers comprising fewer than about 1500 SNP markers is used to determine the contributions of at least 87 canid populations to the test canid genome. In some embodiments, a set of markers comprising fewer than about 200 SNP markers is used to determine the contributions of at least 87 canid populations to the test canid genome.

According to the methods of the invention, the identities of one or both alleles of each marker may be obtained. In some embodiments, the identities of one or both alleles of a marker in a test canid may be determined experimentally using methods that are standard in the art. For example, the identities of one or both alleles of a genomic marker may be determined using any genotyping method known in the art. Exemplary genotyping methods include, but are not limited to, the use of hybridization, Polymerase Chain Reaction (PCR), size fractionation, DNA sequencing, DNA microarrays, high density fiber-optic arrays of beads (see, e.g., Jianbing et al. (2003) *Chin. Sci. Bull.* 48(18):1903-5), primer extension, mass spectrometry (see, e.g., Jurinke et al. (2002) *Meth. Mol. Biol.* 187:179-92), and whole-genome sampling analysis (see, e.g., Kennedy et al. (2003) *Nat. Biotechnol.* 21(10):1233-7). The identities of alleles of markers in a test canid may also have been previously determined and be available from sources such as published literature.

In some embodiments, the genomic DNA of the test canid may be amplified using primers specific for the markers, followed by size analysis or sequencing of the amplification product. Exemplary methods for obtaining the identities of one or both alleles of markers in canid genomes are described in EXAMPLE 1. In some embodiments, the primers used for amplifying genomic DNA containing microsatellite markers are selected from the group consisting of SEQ ID NOs:1-200, although other primers and other microsatellite markers may be used. In some embodiments, the primers used for amplifying genomic DNA containing SNP markers are selected from the group consisting of SEQ ID NOs:244 to 327, although other primers and other SNP markers may be used. The identities of alleles of 68-100 microsatellite markers in 422 canids, including 414 dogs representing 85 breeds, and 8 wolves are set forth in Table 3 (filed herewith on a compact disc). The identities of alleles of 100 SNP markers in 189 canids, including 186 dogs representing 67 breeds, two wolves, and a coyote are set forth in Table 4 (filed herewith on a compact disc).

The minimum number of markers included in the set of markers used in the first step of the methods of the invention depends on the informativeness of the markers for the particular canid populations that are being used. The informativeness of a marker is a function of the number of different alleles within and between the canid populations used in the methods of the invention, the frequency of these alleles, and the rate of mutation rate at the locus. The degree of polymorphism of a genomic locus may be evaluated by an estimation of the polymorphic information content (PIC), which is a function of the number of alleles and their frequency distribution. Exemplary PIC values for microsatellite markers suitable for use in the methods of the invention are set forth in Table 1. Suitable markers for use in the methods of the invention may have an average PIC value of about 0.65%, as shown in EXAMPLE 1.

Methods of determining the number of alleles of markers in different canid populations and their frequencies within and between canid populations are described in EXAMPLE 1. For example, the mean number of alleles per maker, the expected heterozygosity (based on Hardy-Weinberg Equilibrium assumptions), the observed heterozygosity, and the estimated inbreeding coefficients across 95 microsatellite markers in 94 canids, including 90 dogs representing 18 breeds, and 4 wolves, are described in EXAMPLE 1.

The existence of breed barriers would predict that dogs from the same breed should be more similar genetically than dogs from different breeds. To test this prediction, the proportion of genetic variation between individual dogs that could be attributed to breed membership was estimated. Analysis of molecular variance for microsatellite data including 96 markers in 328 dogs representing 68 breeds showed that variation between breeds accounts for more than 27% of total genetic variation, as described in EXAMPLE 1. Similarly, the genetic distance between breeds calculated from SNP marker data including 75 SNPs in 120 dogs representing 60 breeds was F_{ST}=0.36, as described in EXAMPLE 1. These observations are consistent with previous reports that analyzed fewer dog breeds (Koskinen (2003) *Anim. Genet.* 34:297; Irion et al. (2003) *J. Hered.* 94:81), confirming the prediction that breed barriers have led to strong genetic isolation among breeds, and are in striking contrast to the much lower genetic differentiation (typically in the range of 5-10%) found between human populations (Rosenberg et al. (2002) *Science* 298:2381-5; Cavelli-Sforza et al. (1994) *The History and Geography of Human Genes*, Princeton University Press, Princeton). Variation among breeds in dogs is on the high end of the range reported for livestock populations (MacHugh et al. (1998) *Anim. Genet.* 29:333; Laval et al. (2000) *Gen. Sel. Evol.* 32:187). Strong genetic differentiation among dog breeds indicates that breed membership may be determined from genotype information for individual canids.

The influence of the number of distinct alleles of a marker in a dataset on the informativeness of the marker is shown in EXAMPLE 2. For example, in an analysis of 19 canid populations and 95 microsatellite markers, 86% of canids were correctly assigned to their breed using 5 markers that each had more than 10 distinct alleles, and 95% of canids were correctly assigned using 10 or more markers that each had more than 10 distinct alleles. For markers with 1-3 distinct alleles, 46% of canids were correctly assigned to their breed using 5 markers, and 62% of canids were correctly assigned using 10 or more markers.

The influence of the number of markers used on the ability to discriminate between 19 canid populations using genotype information for 95 markers for 4 or 5 canids per canid population is shown in EXAMPLE 2. For example, the minimum number of markers required to successfully assign 100% of individuals to the correct canid population ranged between 2 (Pekingese) and 52 (American Hairless Terrier) depending on the canid population. The minimum number of microsatellite markers required to successfully assign at least 90% of all 94 tested individuals across the 19 canid populations, with the chosen canid population having 100% accuracy, ranged between 8 (for Pekingese) to 95 (for Preso Canario, Chihuahua, and American Hairless Terrier).

The second step of the methods of the first aspect of the invention comprises determining the contributions of canid populations to the test canid genome by comparing the alleles in the test canid genome to a database comprising canid population profiles, wherein each canid population profile comprises genotype information for alleles of the markers in the set of markers in the canid population. A "canid population profile" as used herein refers to the collection of genotype information for the set of markers in a canid population. Thus, a canid population profile may comprise genotype information for most or all alleles of most or all markers in the set of markers in the canid population. For example, a canid population profile may comprise genotype information for each allele of each marker in the set of markers in the canid population. The genotype information in a canid population profile may comprise information such as the identity of one or both alleles of most or all of the markers in the set of markers in one or more canids that are members of that canid population, and/or estimated allele frequencies for at least one allele of most or all of the markers in the set of markers in that canid population. An "allele frequency" refers to the rate of occurrence of an allele in a population. Allele frequencies are typically estimated by direct counting. Generally, allele frequencies in a canid population are estimated by obtaining the identity of one or both alleles for each of the set of markers in at least about five members of that canid population. A "database of canid population profiles" refers to the collection of canid population profiles for all of the canid populations used in an exemplary method of the invention. In some embodiments, the database of canid population profiles comprises between about five and about 500 canid population profiles, such as about 20 canid population profiles, about 50 canid population profiles, or about 100 canid population profiles.

Determining the contributions of canid populations to the test canid genome encompasses both assigning a canid genome to a particular canid population and determining the fraction of the canid genome that was derived from one or more canid populations. In some embodiments of the method, a Bayesian model-based clustering approach is used. There are two broad classes of clustering methods that are used to assign individuals to populations (Pritchard et al. (2000) *Genetics* 155:945-59). Distance-based methods calculate a pairwise distance matrix to provide the distance between every pair of individuals. Model-based methods proceed by assuming that observations from each cluster are random draws from some parametric model; inference for the parameters corresponding to each cluster is then done jointly with inference for the cluster membership of each individual, using standard statistical methods. Any standard statistical method may be used in the methods of the invention, including maximum likelihood, bootstrapping methodologies, Bayesian methods and any other statistical methodology that can be used to analyze genotype data. These statistical methods are well-known in the art. Many software programs for population genetics studies have been developed and may be used in the methods of the invention, including, but not limited to TFPGA, Arlequin, GDA, GENEPOP, GeneStrut, POPGENE (Labate (2000) Crop. Sci. 40:1521-1528), and structure (Pritchard et al. (2000) *Genetics* 155:945-59).

An exemplary Bayesian model-based clustering approach is provided by the genotype clustering program structure (Pritchard et al. (2000) *Genetics* 155:945-59), which has proven useful for defining populations within a species (Rosenburg et al. (2001) *Genetics* 159:699-713; Rosenburg et al. (2002) *Science* 298:2381-5; Falush et al. (2003) *Genetics* 164(4):1567-87). The clustering method used by structure requires no prior information about either phenotype or genetic origin to accurately place an individual or set of related individuals in a population.

Any algorithms useful for multi-locus genotype analysis may be used in the methods of the invention, for example, classic assignment algorithms. Suitable algorithms include those described in Rannala & Mountain (1997) *Proc. Natl. Acad. Sci. U.S.A.* 94:9197-9201 and Cornuet et al. (1999) *Genetics* 153:1989-2000 and variations thereof. Exemplary programs available for multi-locus genotype analysis include Doh (available at www2.biology.ualberta.ca/jbrzusto/Doh.php) and GeneClass (available at www.montpellier.inra.fr/URLB/geneclass/genecass.htm).

In some embodiments, the methods of the invention comprise determining the probability that a specific canid population contributed to the genome of the test canid by determining the conditional probability that the alleles in the test canid genome would occur in the specific canid population divided by the sum of conditional probabilities that the alleles in the test canid genome would occur in each canid population in the database.

Some embodiments of the methods of the invention comprise discriminating between the contributions of two or more genetically related canid populations to the test canid genome by comparing the alleles in the test canid genome to a database comprising profiles of the two or more genetically related canid populations. The two or more genetically related canid populations may comprise Belgian Sheep Dog and Belgian Tervuren; Collie and Shetland Sheep Dog; Whippet and Greyhound; Siberian Husky and Alaskan Malamute; Mastiff and Bullmastiff; Greater Swiss Mountain Dog and Bernese Mountain Dog; West Highland White Terrier and Cairn Terrier; or Lhasa Apso, Shih Tzu, and Pekinese.

Using an assignment algorithm on genotype information for 95 microsatellite markers from 94 canids, including 90 canids representing 18 breeds and 4 wolves, the methods of the invention have been used to assign each individual canid to its breed with 99% accuracy, as described in EXAMPLE 2. A clustering algorithm used on the same genotype information predicted 20 canid populations and assigned each canid to one population with 99% accuracy, as described in EXAMPLE 3.

Using an assignment algorithm on genotype information for 68 microsatellite markers from 341 canids representing 72 breeds, the methods of the invention have been used to assign 96% of the canids to the correct breed, as described in EXAMPLE 2. Using an assignment algorithm on genotype information for 96 microsatellite markers from 414 canids representing 85 breeds, the methods of the invention have been used to assign 99% of the canids to the correct breed, as described in EXAMPLE 4. Similar results were obtained using a clustering algorithm. Using an assignment algorithm on genotype information for 100 SNP markers from 189 canids representing 67 breeds, the methods of the invention have been used to assign 80% of canids to the correct breed with a probability of 99% of greater, as described in EXAMPLE 6.

The methods of the invention are also useful for determining the contributions of canid populations to mixed-breed canids. Admixed individuals represent approximately 50% of the canine population. Models that detect an individual's admixed state can be considered to group into two classes: models that require a combinatoric set of unique alleles for each of the possible mixtures of ancestral populations (Nason & Ellstrand (1993) *J. Hered.* 84: 1-12; Epifanio & Philipp

(1997) *J. Hered.* 88:62-5), and Bayesian methods where ancestral populations are not required to contain a combination describing unique alleles, but instead assign individuals to admixed states probabilistically based on differences in allele frequencies between populations (Corander et al. (2003) *Genetics* 163(1): 367-74; Anderson & Thompson (2002) *Genetics* 160:1217-29, Pritchard et al. (2000) *Genetics* 155:945-59, Rannala & Mountain (1997) *Proc. Natl. Acad. Sci. U.S.A.* 94:9197-9201. The latter set of models are more informative for most populations and data sets as they allow for a Bayesian posterior probabilistic assignment vector for each population/generation combination, thereby allowing for uncertainty analysis to be incorporated into the assignment vector; but existing models for the exact, recent admixture assignments of individuals from multiple ancestral populations are limited in their scope as they have been developed thus far only for two generation prediction and allow for only a few ancestral populations. For example, the methods of Anderson & Thompson (2002) are developed for a two generation, two population model with unlinked microsatellite data. A naïve Bayesian classification model that incorporates linked and unlinked microsatellite loci information, higher-dimensioned ancestral populations, and higher-ordered generation pedigrees for the probabilistic assignment of individuals to mixtures of ancestral subpopulations is described in EXAMPLE 7. This model simultaneously addresses the generation, subpopulation, and linkage limitations of previous models, and 2- and 3-generational models have been implemented for exact admixture detection and assignment, as described in EXAMPLE 7.

Using a clustering algorithm on in silico mixes of genotype information for 95 markers from 85 canids, consisting of 81 canids representing 18 breeds and 4 wolves, the methods of the invention have been used to identify in silico mixing at the parent level with 100% accuracy, as described in EXAMPLE 5. The methods of the invention were also highly accurate at detecting in silico mixing at the grandparent level, and fairly accurate at detecting in silico mixing at the great-grandparent level, as shown in EXAMPLE 5. Thus, the methods of the invention may be used to discriminate mixes at the parent and grandparent level from pure-bred dogs (as well as ½ wolf and ¼ wolf mixes from dogs) and identify breed contributions in the genome of a mixed-breed dog.

Using a Bayesian classification model on in silico mixes of genotype information for 96 markers from 429 canids representing 88 breeds, the methods of the invention have been used to correctly assign more than 98% of F1 mixes and more than 94% of F2 mixes, as described in EXAMPLE 7. Using this model on genotype information for 72 markers from 160 known mixed-breed canids, the methods of the invention have been used to correctly assign more than 96% of F1 mixes and more than 91% of F2 mixes, as described in EXAMPLE 7.

The methods of the invention may further comprise the step of providing a document displaying the contributions of one or more canid populations to the genome of the test canid genome. The term "document" refers to a chart, certificate, card, or any other kind of documentation. The document may display the contributions of one or more canid populations to the test canid genome in a numeric format or in a graphic format. For example, the document may include photographs or other depictions, drawings, or representations of the one or more canid populations. The document may also provide confidence values for the determined contributions (such as 80%, 85%, 90% 95%, or 99% confidence). In some embodiments, the document provides a certification of the contributions of one or more canid populations to the genome of the test canid genome.

In some embodiments, the document additionally provides information regarding the one or more canid populations that contributed to the genome of the test canid or the test canid. The information regarding canid populations that contributed to the genome of the test canid may include information related to the characteristics and origin of the canid population or any other kind of information that would be useful to the owner of the test canid. In some embodiment, the information includes health-related information. Many canid populations have predispositions to particular diseases or conditions. For example, Afghan hounds are predisposed to glaucoma, hepatitis, and hypothyroidism; Basenji are predisposed to coliform enteritis and pyruvate kinase deficiency; Beagles are predisposed to bladder cancer and deafness; Bernese Mountain dogs are predisposed to cerebellar degeneration; Border Terriers are predisposed to oligodendroglioma; and Labrador Retrievers are predisposed to food allergies (see, e.g., Dr. Bob's All Creatures Site, Breed Predisposition to Disease and Congenital Conditions; Patterson et al. (1988) *J. Am. Vet. Med. Assoc.* 193:1131). Of the genetic diseases discovered in dogs, 46% are believed to occur predominantly or exclusively in one or a few breeds (Patterson et al. (1988) *J. Am. Vet. Med. Assoc.* 193:1131.) Therefore, information regarding the contributions of one or more canid populations to the genome of the test canid genome is particularly valuable to mixed-breed canid owners or caretakers (both professional and non-professional) for the purpose of proactively considering health risks for individual tested animals. For example, a mixed breed dog that is found to be a mixture of Newfoundland and Bernese Mountain Dog should be actively monitored for genetic diseases that occur with rare frequency in the general population of dogs, but occur with significant frequency in these specific breeds; thus, a mixed-breed individual of this type would benefit from screens for malignant histiocytosis (disease heritability of 0.298 in Bernese Mountain dogs, Padgett et al. 1995 *J. Small Anim. Pract.* 36(3):93-8) in addition to Type I cystinuria genetic screens (nonsense mutation isolated in Newfoundlands at exon 2 of SLC3A1 gene, Henthorn et al. (2000) *Hum. Genet.* 107(4):295-303).

Health-related information may also include potential treatments, special diets or products, diagnostic information, and insurance information. An exemplary document displaying the contributions of one or more canid populations to the genome of a test canid is shown in FIG. **1**.

In some embodiments, the invention provides methods for defining one or more canid populations, comprising: (a) for each of a set of canid genomes, obtaining the identity of one or both alleles for each of a set of markers; and (b) defining one or more canid populations by determining the likelihood that one or more members of the set of canid genomes define distinct canid populations characterized by a set of allele frequencies for each marker. Exemplary methods of the invention for defining one or more canid populations are described in EXAMPLES 3 and 4.

In another aspect, the invention provides substrates comprising nucleic acid sequences for determining the identity of one or both alleles in a canid genome for each of a set of markers. The substrates may be in any form suitable for determining the identity of alleles of markers. For example, the substrate may be in the form of a microarray or a collection of beads.

In a further aspect, the invention provides a computer-readable medium comprising a data structure stored thereon for use in distinguishing canid populations, the data structure comprising: a marker field, which is capable of storing the name of a marker (for example, an SNP marker) or the name of an allele of a marker; and a genotype information field, which is capable of storing genotype information for the marker (for example, the identity of one or both alleles of the marker in a canid genome or an estimate of the frequency of an allele of the marker in a canid population), wherein a record comprises an instantiation of the marker field and an instantiation of the genotype information field and a set of records represents a canid population profile.

A "computer-readable medium" refers to any available medium that can be accessed by computer and includes both volatile and nonvolatile media, removable and non-removable media. By way of example, and not limitation, computer-readable media may comprise computer storage media and communication media. Computer storage media includes both volatile and nonvolatile, removable and non-removable media implemented in any method or technology for storage of information, such as computer-readable instructions, data structures, program modules, or other data. Computer storage media include, but are not limited to, RAM, ROM, EEPROM, flash memory or other memory technology, CD-ROM, digital versatile disks (DVD) or other optical disk storage, magnetic cassettes, magnetic tapes, magnetic disk storage or other magnetic storage devices, or any other computer storage media. Communication media typically embody computer-readable instructions, data structures, program modules or other data in a modulated data signal, such as a carrier wave or other transport mechanism that includes any information delivery media. The term "modulated data signal" means a signal that has one or more of its characteristics set or changed in such a manner as to encode information in the signal. By way of example, and not limitation, communication media include wired media, such as a wired network or direct-wired connection, and wireless media, such as acoustic, RF infrared, and other wireless media. A combination of any of the above should also be included within the scope of computer-readable media.

A "data structure" refers to a conceptual arrangement of data and is typically characterized by rows and columns, with data occupying or potentially occupying each cell formed by a row-column intersection. The data structure in the computer-readable medium of the invention comprises a marker field and a genotype information field, as described above. The instantiation of the marker field and the genotype information field provides a record, and a set of record provides a canid population profile. Thus, the data structure may be used to create a database of canid population profiles.

In some embodiments, the computer readable medium comprises a substrate having stored thereon: (a) a data structure for use in distinguishing canid populations, the data structure comprising: (i) a marker field, which is capable of storing the name of a marker or of an allele of a marker; and (ii) a genotype information field, which is capable of storing genotype information for the marker, wherein a record comprises an instantiation of the marker field and an instantiation of the frequency field and a set of records represents a canid population profile; and (b) computer-executable instructions for implementing a method for determining the contributions of canid populations to a canid genome, comprising: (i) obtaining the identity of one or both alleles in a test canid genome for each of a set of markers; and (ii) determining the contributions of canid populations to the test canid genome by comparing the alleles in the test canid genome to a database comprising canid population profiles, wherein each canid population profile comprises genotype information for the set of markers in the canid population.

The following examples merely illustrate the best mode now contemplated for practicing the invention, but should not be construed to limit the invention.

Example 1

This example describes a representative method of the invention for obtaining the identity of one or both alleles for a set of markers and selecting markers suitable for determining the contribution of canid populations to the genome of a canid.

A. Methods

1. Sample Collection and DNA Extraction

Canid DNA samples from 513 American Kennel Club-registered dogs representing 103 breeds and 8 gray wolves from eight countries (China, Oman, Italy, Iran, U.S.A. (Alaska), Canada (Quebec), Sweden, Mexico) were obtained by collecting buccal (cheek) swabs and/or blood samples from volunteers at dog shows and dog club specialty events, as well as by mail-in donations. American Kennel Club registration number and detailed pedigree information was requested for all dogs, as participation was limited to unrelated dogs that did not share grandparents. Pedigree information was also collected for 84% of sampled individuals. In many cases, five-generation pedigrees were obtained, and while dogs sometimes appear redundantly at the great-grandparent level or higher, inspection of the complete lineage indicates a high degree of unrelatedness among dogs of the same breed. For those individuals where a pedigree was not available, unrelatedness was verified by breed club representatives. Each individual canid was given a canid identification number. Abbreviations used for breeds and other canid populations are shown in Table 5. In addition DNA samples from 160 mixed-breed canids comprising admixture components from 20 AKC breeds were obtained by collecting buccal swabs.

Buccal swabs were collected in a manner similar to that suggested by the American Kennel Club (AKC) website using cytology brushes (Medical Packaging Corp., Camarillo, Calif.). DNA was extracted from buccal swabs using QiaAmp blood kits following manufacturers' protocol (Qiagen, Valencia, Calif.). DNA extraction from blood was done as described previously (Comstock et al. (2002) *Mol. Ecol.* 11:2489-98).

2. Analysis of Microsatellite Markers

One hundred dinucleotide microsatellite markers were chosen from the 1596 microsatellites currently localized on the 3300 marker map of the dog (Guyon et al. (2003) *Proc. Natl. Acad. Sci U.S.A.* 100(9):5296-5301) (Table 1). Markers were selected based on informativeness, calculated as a PIC, value, and distribution across all 38 autosomes. Selected markers had an average PIC value of 0.65% (range 36%-86%) and an average spacing of 29.5 Mb (range 21.5-50.9 Mb). Dinucleotide, rather than tetranucleotide microsatellites were chosen to reduce the number of spurious mutations observed that could hamper breed identification.

DNA samples were arrayed on five 96-well plates. A positive control was included on each plate to ensure consistent allele binning. PCR was performed in 10 microliter reactions containing 1 ng of genomic DNA and final concentrations of the following reagents: 16 mM ammonium sulfate, 67 mM Tris-HCl pH 8.8, 2.0 mM $MgCl_2$, 0.1 mM dNTPs, 300 nM forward primers (SEQ ID NOs:1-100), reverse primers (SEQ ID NOs:101-200), and dye-labeled M13 Primers (PE Applied Biosystems, Foster City, Calif. USA). Forward primers were redesigned to include a 19 base M13 forward (−29) sequence,

5'-CACGACGTTGTAAAACGAC-3' (SEQ ID NO:201), on the 5 prime end. Samples were labeled by the addition of 0.25 pmol of an M13 primer (SEQ ID NO:201) tagged with either 6FAM™, VIC™, NED™ or PET™ (ABI, Foster City, Calif.) dyes to each reaction. PCR incubation was carried out according to standard protocols (see, e.g., Lowe et al. (2003) *Genomics* 82: 86-95). Annealing temperatures used are provided in Table 1. Four samples labeled with different dyes were multiplexed following completion of PCR by combining 3 microliters of each reaction mix into a single 96 well plate. Samples were denatured in 2 volumes Hi-Di™ formamide with 16 pmol of GeneScan™-500LIZ™ size standard (ABI, Foster City, Calif.) according to manufacturers' protocols. All samples were loaded on an ABI 3730 DNA Analyzer™ (PE applied Biosystems) capillary electrophoresis instrument for allele separation. Genotypes were called using GeneMapper™ v3.0 software (ABI, Foster City, Calif.). All calls were checked manually and each subsequent run was scanned for the appearance of new alleles outside existing bins. Four markers failed to amplify consistently and were discarded.

3. SNP Discovery and Genotyping

Fifty canine bacterial artificial chromosomes (BACs) were chosen at random from the canine radiation hybrid map (Guyon et al. (2003) *Proc. Natl. Acad. Sci U.S.A.* 100(9): 5296-5301). The Primer3 program described in Krawetz S, Misener S (eds) *Bioinformatics Methods and Protocols: Methods in Molecular Biology*. Humana Press, Totowa, N.J., pp 365-386 was used to design primers from each BAC end sequence. The resulting amplicons averaged 334 base pairs. Primers were used to amplify 19867 base pairs of non-continuous genomic sequence in 189 dogs representing 67 domestic dog breeds, coyote, and the gray wolf. The resulting PCR products were sequenced using standard methods on an ABI 3700 capillary sequencer with standard ABI dye terminator chemistry (ABI, Foster City, Calif.) and resequence. All sequence reads were aligned and viewed using Phred, Phrap and Consed (Ewing & Green (1998)*Genome Res.* 8:186-94; Ewing et al. (1998) *Genome Res.* 8:175-85; available at www.genome.washington.edu). The computer program Polyphred was used to identify regions of polymorphism, both SNP and insertion/deletion, within and between sequence reads (Nickerson et al. (1997) *Nucl. Acids Res.* 25:2745-51, available at droog.mbt.washington.edu). All allele calls were confirmed manually and confirmed through visual inspection of the traces.

4. Statistical Analysis

An analysis of molecular variance (AMOVA) was performed with GDA (Lewis & Zaykin (2001) Genetic Data Analysis: Computer Program for the Analysis of Allelic Data, Version 1.0 (d16c) under assumption of Hardy-Weinberg equilibrium. Similar results were obtained for the fraction of genetic variation among breeds when inbreeding was allowed for in the analysis.

Expected heterozygosity for each breed was calculated from allele frequencies using Tajima's unbiased estimator (Tajima (1989) *Genetics* 123:585-95).

B. Results

1. Informativeness of Dinucleotide Microsatellites

The identities of alleles (length of the amplified region) of 68-100 microsatellite markers in 422 canids, including 414 dogs representing 85 breeds, and 8 wolves, are set forth in Table 3 (filed herewith on a compact disc). 148 alleles were found to be unique to a specific canid population: 1 each to ACKR, AUST, BORD, BOX, BULD, DACH, GOLD, GSHP, GSMD, IBIZ, KEES, NELK, PEKE, POM, ROTT, SFXT, TERV, and WHIP, 2 each to BEAG, CAIR, HUSK, IRSE, MAST, OES, SCHP, SCWT, SPOO, and SSHP, 3 each to AMAL, BMD, KOMO, NEWF, STBD, and WSSP, 4 each to KUVZ, PNTR, and PRES, 5 each to BSJI and SHAR, 6 to AKIT, and 64 to WOLF.

Six different datasets were used for subsequent analyses, as further described in EXAMPLES 2-5 and 7. The first dataset included genotype information for 95 microsatellite markers (microsatellite markers 1-14, 16, 18-21, 23-36, 39-100, see Table 1) in 94 canids, including 90 canids representing 18 breeds and 4 wolves (dataset 1, Table 6). The second dataset included genotype information for 68 microsatellite markers (microsatellite markers 2-8, 11, 12, 14-16, 18-21, 23, 24, 26-32, 34-36, 38, 41, 42, 44-46, 50, 51, 53, 54, 56, 60-64, 67, 68, 70-74, 78, 79, 81-83, 85, 87-91, 93-98, see Table 1) in 341 canids representing 72 breeds (dataset 2, Table 7). The third dataset included genotype information for 96 microsatellite markers (microsatellite markers 1-9, 11-38, 40-42, 44-75, 77-100, see Table 1) in 414 canids representing 85 breeds (dataset 3, Table 8). The fourth dataset included genotype information for 96 microsatellite markers (microsatellite markers 1-9, 11-38, 40-42, 44-75, 77-100, see Table 1) in 85 canids, including 81 dogs representing 18 breeds, and 4 wolves (dataset 4, Table 9). The fifth dataset included genotype information for 96 microsatellite markers (microsatellite markers 1-9, 11-38, 40-42, 44-75, 77-100, see Table 1) in 429 canids representing 88 breeds. The sixth dataset included genotype information for 72 of the microsatellite markers in Table 1 in 160 mixed-breed canids, as set forth in Table 3 (filed herewith on a compact disc).

The proportion of polymorphic markers, the mean number of alleles per maker, the mean number of alleles per polymorphic maker, the expected heterozygosity (based on Hardy-Weinberg Equilibrium assumptions), the observed heterozygosity, and the estimated inbreeding coefficients across 95 microsatellite markers in dataset 1 are shown in Table 10. The expected heterozygosity of 85 canid populations averaged over 96 microsatellites (dataset 3) using Tajima's unbiased estimator is shown in Table 11.

The existence of breed barriers would predict that dogs from the same breed should be more similar genetically than dogs from different breeds. To test this prediction, the proportion of genetic variation between individual dogs that could be attributed to breed membership was estimated. Analysis of molecular variance in the microsatellite data for 96 microsatellites in 414 dogs representing 85 breeds (dataset 3, Table 8) showed that variation between breeds accounts for more than 27% of total genetic variation.

2. Informativeness of SNP Markers

Using 189 canids representing 67 domestic breeds, coyote and wolf, 100 polymorphic sites in approximately 20 Kb of non-continuous canine genomic sequence were identified, as shown in Table 2. These include 92 single base substitutions and 11 insertion or deletion mutations ranging from one to eight nucleotides in length. The identities of alleles for 100 SNP markers in 189 canids, including 186 dogs representing 67 breeds, two wolves, and a coyote are set forth in Table 4 (filed herewith on a compact disc). Minor allele frequencies in 75 SNPs from 120 dogs representing 60 breeds ranged from 0.4% to 48%, as shown in Table 2. Fourteen of these SNPs were breed-specific: 372c5t-82 (English Shepherd), 372e13t-57 (Cocker Spaniel), 372m6t-88 (English Shepherd), 372m23t-76 (Alaskan Malamute), 373a15t-112 (Chesapeake Bay Retriever), 373e1t-50 (Spinoni Italiano), 373e1t-130 (Scottish Deerhound), 373g19t-246 (Borzoi), 373i8s-224 (Chesapeake Bay Retriever), 373k8s-181 (Tibetan Terrier), 372c5s-168 (Akita), 372C15S-196 (Labrador Retriever), 372e15s-71 (Field Spaniel), 373a21t-93 (Italian Greyhound).

When all dogs were considered as a single population, the observed heterozygosity (Tajima & Nei (1984) *Mol. Biol. Evol.* 1:269-85) was 8×10^{-4}, essentially the same as that seen in the human population (Sachidanandam et al. (2001) *Nature* 409:928-33; Venter et al. (2001) *Science* 291:3104-51). However, when the breeds are separated, there is a 4-fold range in heterozygosity between the least outbred (Scottish Deerhound, 2.5×10^{-4}) to most outbred (English Shepherd, 1.0×10^{-3}). The genetic distance between breeds calculated from the SNP data for 75 SNPs in 120 dogs representing 60 breeds was $F_{ST}=0.36$.

The expected heterozygosity of 60 canid populations based on allele frequencies at 75 SNP loci (dataset 3) using Tajima's unbiased estimator is shown in Table 12. Each breed is represented by 2 dogs.

Example 2

This example describes a representative method of the invention for estimating the contributions of canid populations to a canid genome using an assignment test calculator on genotype information for 95 microsatellite markers from 94 canids, and on genotype information for 68 microsatellite markers from 341 canids.

A. Methods

1. Datasets

Dataset 1 included genotype information for 95 microsatellite markers from 94 canids, including 90 dogs representing 18 breeds, and 4 wolves (AHRT, AKIT, BEAG, BMD, BOX, BULD, BULM, CHIH, DACH, GOLD, IBIZ, MAST, NEWF, PEKE, POM, PRES, PUG, ROTT, WOLF, see Table 5 for abbreviations of canid populations). The 95 microsatellite markers were microsatellite markers 1-14, 16, 18-21, 23-36, 39-100 (Table 1). The dataset contained genotype information from 5 canids for each breed and 4 wolves (Table 6). The genotype information for the canids in dataset 1 is set forth in Table 3 (filed herewith on a compact disc).

Dataset 2 included genotype information for 68 markers from 341 canids representing 72 breeds (ACKR, AFGH, AHRT, AIRT, AKIT, AMAL, AMWS, AUSS, AUST, BASS, BEAG, BEDT, BELS, BLDH, BMD, BORD, BORZ, BOX, BSJI, BULD, BULM, CAIR, CHBR, CHIH, CKCS, CLSP, COLL, DACH, DANE, DNDT, DOBP, ECKR, FCR, GOLD, GREY, GSD, GSHP, GSMD, HUSK, IBIZ, IRSE, IRTR, IWOF, KEES, KOMO, KUVZ, LAB, MAST, MBLT, MNTY, NELK, NEWF, OES, PEKE, PNTR, POM, PRES, PTWD, PUG, RHOD, ROTT, SCHP, SCWT, SFXT, SHAR, SPOO, SSHP, STBD, TERV, WHIP, WHWT, WSSP, see Table 5 for abbreviations of canid populations). The 68 microsatellite markers were microsatellite markers 2-8, 11, 12, 14-16, 18-21, 23, 24, 26-32, 34-36, 38, 41, 42, 44-46, 50, 51, 53, 54, 56, 60-64, 67, 68, 70-74, 78, 79, 81-83, 85, 87-91, 93-98 (Table 1). The dataset contained genotype information from 5 canids for each breed, except for SFXT (2 canids), ACKR, AFGH, DNDT, OES (3 canids each), AIRT, BASS, BEDT, IRTR, MNTY, SCHP, SCWT, and TERV (4 canids each) (Table 7). The genotype information for the canids in dataset 2 is set forth in Table 3 (filed herewith on a compact disc).

2. Doh Analysis

The assignment test calculator Doh was used as described in Paetkau D. et al., Molecular Ecology 4: 347-354 (1995) for an analysis of the two datasets of genotype information. All individual canids were designated with their known population except for the canid to be tested, which was then assigned by the program to the canid population with the highest probability of generating the test canid's genotype. The program repeats this procedure with each canid as test canid.

B. Results

1. Doh Analyses Using Dataset 1

Using Doh on the genotype information in dataset 1, including genotype information for 95 microsatellite markers in 94 canids (90 dogs representing 18 breeds, and 4 wolves), 99% of the canids were assigned to the correct canid population. 100% canids were correctly assigned for the following breeds: AHRT, AKIT, BEAG, BMD, BOX, BULD, CHIH, DACH, GOLD, IBIZ, MAST, NEWF, PEKE, POM, PUG, ROTT, WOLF. The only canid that was misassigned was one dog (out of 5 dogs) of the Presa Canario breed. The misassigned Presa Canario dog was assigned to Chihuahua.

It was found that the discrimination power of the allelic patterns depended on the number of independent microsatellite loci, the allelic diversity at each locus, and the number of individuals sampled from each breed. To evaluate the effect of the number of alleles of a marker and the number of markers on informativeness of that marker, a Doh assignment analysis for the first 19 breeds was performed with 5, 10, 15, and 20 markers, binning markers with 1-3 distinct alleles found in the dataset, 4-6 distinct alleles, 7-10 distinct alleles, and more than 10 distinct alleles. For the bins that did not contain 20 markers, the maximum number of markers was used. For markers with more than 10 distinct alleles, 86% of canids were correctly assigned to their breed using five markers, and 95% of canids were correctly assigned using 10, 15, or 20 markers. For markers with 7-10 distinct alleles, 84% of canids were correctly assigned to their breed using 5 markers, and 91% of canids were correctly assigned using 10 markers, and 94% of canids were correctly assigned using 15, or 20 markers. For markers with 4-6 distinct alleles, 62% of canids were correctly assigned to their breed using 5 markers, and 71% of canids were correctly assigned using 10, 15, or 20 markers. For markers with 1-3 distinct alleles, 46% of canids were correctly assigned to their breed using 5 markers, and 62% of canids were correctly assigned using 10, 15, or 20 markers.

The minimum number of microsatellite markers found in a 2-class (0-1) directed search of the allele frequency patterns within the 95 markers required to successfully assign 100% of the individuals to the correct canid populations (incorrect assignment is to any other breed) was 2 for PEKE, 3 for BOX, POM, and WOLF, 4 for AKIT, MAST, and PUG, 5 for NEWF and ROTT, 6 for BMD, 8 for BEAG, 11 for IBIZ, 12 for GOLD, 17 for DACH, 19 for BULD, 26 for BULM, 44 for PRES, 49 for CHIH, and 52 for AHRT. There is a positive correlation between the minimum number of microsatellite markers required for 100% (0-1) discrimination, and the mean number of alleles across the 95 microsatellite markers for the 94 canids tested in 19 canid populations (see Table 10).

The minimum number of microsatellite markers found in a multiclass (0, 1, 2, . . . 18) directed search of the allele frequency patterns within the 95 markers required to successfully assign at least 90% of all 94 tested individuals across the 19 canid populations, with the chosen canid population having 100% accuracy, was 8 for PEKE, BOX, POM, WOLF, AKIT, MAST, PUG, NEWF, ROTT, and BMD, 11 for BEAG, 14 for IBIZ, 14 for GOLD, 23 for DACH, 24 for BULD, 28 for BULM, and 95 for PRES, CHIH, and AHRT.

As expected, the discrimination power reflects the level of inbreeding observed in each breed. For example, certain breeds have allelic variation 3-fold less than the average breed allelic variation and those breeds have both higher discrimination power and the characteristic population dynamics of long population bottlenecks and small effective population sizes

2. Doh Analysis Using Dataset 2

Using Doh on the genotype information in dataset 2, including genotype information for 68 markers from 341 canids representing 72 breeds, 96% of the dogs tested were assigned to the correct breed, as shown in Table 13. If both Belgian breeds (Belgian Sheepdog and Belgian Tervuren) were counted as one breed, 98% of the dogs tested were assigned to the correct breed.

Example 3

This example describes a representative method of the invention for estimating the contributions of canid populations to a canid genome using cluster analysis on genotype information for 95 microsatellite markers from 94 canids.

A. Methods

1. Dataset

Dataset 1 included genotype information for 95 microsatellite markers from 94 canids, including 90 dogs representing 18 breeds, and 4 wolves, as described in EXAMPLE 2.

2. Cluster Analysis

Cluster analysis was performed using the multilocus genotype clustering program structure (Pritchard et al. (2000) *Genetics* 155:945-59; Falush et al. (2003) *Science* 299:1582-5), which employs a Bayesian model-based clustering algorithm to identify genetically distinct subpopulations based on patterns of allele frequencies. Multiple runs were completed for each value of K (number of genetic clusters) with burn-in lengths of 10,000 steps and 100,000 iterations of the Gibbs sampler. The correlated allele frequency model was used with asymmetric admixture allowed. All values of K from 2 to 80 were tested and the clustering solutions that produced the highest likelihood were retained for further verification. To choose the overall best clustering solution for the data set, an all-pairs Wilcoxon two-sample test was performed for the 5 highest likelihood values of K.

3. Nested Set Clustering

Starting with the complete data set, all individuals were hierarchically divided into sub-clusters where each (K+1)th sub-cluster was created by splitting one of the previous K clusters based on the highest observed likelihood value across 10 runs. Employing a hierarchical method for deriving clusters of individuals may infer a reasonable methodology for ascertaining population phylogeny when genetic variability between sub-populations is reduced due to a modified amount of admixture.

B. Results

A maximum likelihood calculation using structure predicted 20 populations in dataset 1 (95 markers in 19 canid populations) and assigned each individual to one group with 99% accuracy, as shown in Table 14. The one individual that was not assigned to its breed group was a single Presa Canario, which was placed between the Bulldog and the Bullmastiff groups. The Presa Canario is a recreated breed that has been developed through admixture of various mastiff types. The misassigned dog, in particular, can trace its heritage to both a bulldog and a Bullmastiff within the last 12 generations.

The clustering assignment was not able to distinguish between the Bullmastiffs and the Mastiffs at this level of analysis but this was solved by nested analysis, as shown in Tables 15A-D. In the nested analysis, the same clustering algorithms were applied in a stepwise fashion. First, the entire set was divided into two populations. Based on maximum likelihood, one of these two populations was then divided into two to provide a total of three populations. This process was repeated until all populations were resolved. The divisions from five to nine groups clearly show the relationships between the mastiff type breeds. This relationship and the hierarchy predicted conforms perfectly to that expected from breed accounts.

Example 4

This example describes a representative method of the invention for estimating the contributions of canid populations to a canid genome using cluster analysis on genotype information for 96 microsatellite markers in 85 canid populations.

A. Methods

1. Dataset

Dataset 3 included genotype information for 96 markers from 414 canids representing 85 breeds (ACKR, AFGH, AHRT, AIRT, AKIT, AMAL, AMWS, AUSS, AUST, BASS, BEAG, BEDT, BELS, BICH, BLDH, BMD, BORD, BORZ, BOX, BSJI, BULD, BULM, CAIR, CHBR, CHIH, CHOW, CKCS, CLSP, COLL, DACH, DANE, DOBP, ECKR, FBLD, FCR, GOLD, GREY, GSD, GSHP, GSMD, GSNZ, HUSK, IBIZ, IRSE, IRTR, ITGR, IWOF, KEES, KERY, KOMO, KUVZ, LAB, LHSA, MAST, MBLT, MNTY, MSNZ, NELK, NEWF, OES, PEKE, PHAR, PNTR, POM, PRES, PTWD, PUG, RHOD, ROTT, SALU, SAMO, SCHP, SCWT, SHAR, SHIB, SHIH, SPOO, SSHP, SSNZ, STBD, TIBT, TERV, WHIP, WHWT, WSSP, see Table 5 for abbreviations of canid populations). The 96 microsatellite markers were microsatellite markers 1-9, 11-38, 40-42, 44-75, 77-100 (Table 1). The dataset contained genotype information for 5 canids for all breeds, except for AIRT, BASS, BEDT, BICH, FBLD, IRTR, MNTY, PHAR, SCHP, SCWT, TERV (4 canids each) (Table 8). The genotype information for the canids in this dataset is set forth in Table 3 (filed herewith on a compact disc).

2. Statistical Analyses

Structure was run for 100,000 iterations of the Gibbs sampler after a burn-in of 20,000 iterations. The correlated allele frequency model was used with asymmetric admixture allowed. The similarity coefficient across runs of structure was computed as described (Rosenberg et al. (2002) *Science* 298:2381-5). When the program was run on a partial data set of 68 breeds, it was noted that at values of K above 40 the program created clusters to which no individuals were assigned, and the clusters were unstable from run to run. This is most likely because the algorithm, which was initially designed to separate 2-3 populations, is unable to handle such large numbers of populations simultaneously. Because structure has previously been shown to reliably separate 20 populations (Rosenberg et al. (2001) *Genetics* 159:699-713), the data were divided set into 8 subsets of 10 to 11 breeds each, all possible pairs of these subsets were analyzed. Historically related or morphologically similar breeds were retained in the same subset.

Structure was then applied to the entire data set at K=2 to K=10, with fifteen runs at each K. As K is increased, structure first separates the most divergent groups into clusters, followed by separation of more closely related groups (Rosenberg et al. (2002) *Science* 298: 2381). In the analysis, the likelihood increased with increasing values of K, reflecting additional structure found at each K, but multiple different clustering solutions were found for K>4, and therefore K=2 to

4 were used to describe the global breed structure, with phylogenetic analysis and cluster analysis of subgroups used to define constellations of closely related breeds. Structure runs at K=2-5 were repeated under the no admixture model with similar results. In a separate analysis, eight wolves were added to the structure run at K=2. The wolves were sampled from eight countries: China, Oman, Iran, Italy, Sweden, Mexico, Canada (Ontario) and the United States (Alaska). All wolves clustered together with the first cluster of dog breeds shown in Table 16.

Each breed was assigned to one of the four groups based on breed average majority and structure was run on each group at K=2-4. No additional consistent patterns were observed within the individual groups apart from the reported breed pairs and trio. Outlier analysis was carried out using the software package fdist2. Eleven markers were identified as potential "outliers" with Fst values above the 95th percentile achieved by simulation under the infinite allele model with 85 populations assumed and an average of 10 haploid genotypes per population (Beaumont & Nichols (Dec. 22, 1996) *Proceedings: Biological Sciences* 263: 1619). Assignment and structure analysis performed with these markers removed did not result in significant changes.

For the phylogenetic tree analysis, individual dogs and wolves were assigned to one of 86 populations based on breed or species. Distances between the populations were computed using the program Microsat (E. Minch, A. Ruiz-Linares, D. Goldstein, M. Feldman, L. L. Cavalli-Sforza (1995, 1996)) with the chord distance measure. 500 bootstrap replicates were generated. Neighbor-joining trees were constructed for each replicate using the program Neighbor, and the program Consense was used to create a majority-rule consensus tree. Both of these programs are part of the Phylip package (Felsenstein (1989) *Cladistics* 5: 164). The wolf population was designated as the outgroup in order to root the tree. Wolves from eight different countries were combined into one population for simplicity on the tree shown in FIG. **2**. When taken as individuals, all wolves split off from a single branch, which falls in the same place as the root. The splitting order in the phylogenetic analysis was not correlated with heterozygosity (Table 11), and the twelve breeds that split off first closely mirrored the first cluster identified by structure. These observations argue that the analysis identified a distinct subgroup of genetically related breeds, rather than splitting off idiosyncratic breeds that are unusually inbred or that recently mixed with wild canids.

The assignment test was carried out with the Doh assignment test calculator available from J. Brzustowski as described in Paetkau D. et al., Molecular Ecology 4: 347-354 (1995). All dogs were designated with their known breed except for the one dog to be tested, which was then assigned by the program to the breed with the highest probability of generating the test dog's genotype. The program repeats this procedure with each dog as the test dog. The Belgian Sheepdog and Belgian Tervuren breeds were combined into one designation for this analysis; when they are treated as separate breeds the individual dogs are assigned to one or the other essentially at random.

B. Results

When structure was applied to overlapping subsets of 20-22 breeds at a time, it was observed that most breeds formed distinct clusters consisting solely of all the dogs from that breed, as shown in Table 17. Dogs in only four breeds failed to consistently cluster with others of the same breed: Perro de Presa Canario, German Shorthaired Pointer, Australian Shepherd, and Chihuahua. In addition, six pairs of breeds clustered together in the majority of runs: Belgian Sheepdog and Belgian Tervuren, Collie and Shetland Sheepdog, Whippet and Greyhound, Siberian Husky and Alaskan Malamute, Mastiff and Bullmastiff, and Greater Swiss Mountain Dog and Bernese Mountain Dog. These pairings are expected based on known breed history.

To test whether these closely related breed pairs were nonetheless genetically distinct, structure was applied to each of these clusters. In all but one case the clusters separated into two populations corresponding to the individual breeds, as shown in Table 18. The single exception was the cluster containing Belgian Sheepdogs and Belgian Tervurens. The European and Japanese Kennel Clubs classify them as coat color and length varieties of a single breed (Yamazaki & Yamazaki (1995) *Legacy of the Dog: The Ultimate Illustrated Guide to Over* 200 *Breeds*, Chronicle Books, San Francisco, Calif.; Wilcox & Walkowicz (1995) *Atlas of Dog Breeds of the World*, T.F.H. Publications, Neptune City, N.J.), and while the American Kennel Club recognizes these as distinct breeds, the breed barrier is apparently too recent or insufficiently strict to have resulted in genetic differentiation. This example confirms that the algorithm only separates groups that have true genetic differences (Falush et al. (2003) *Science* 299:1582-5; Pritchard & Rosenberg (1999) *Am. J. Hum. Genet.* 65:200-8).

To test whether a dog could be assigned to its breed based on genotype data alone, the direct assignment method (Paetkau et al. (1995) *Mol. Ecol.* 4:347-54) with a leave-one-out analysis was used. 99% of individual dogs were correctly assigned to the correct breed. Only four dogs out of 414 were assigned incorrectly: one Beagle (assigned to Perro de Presa Canario), one Chihuahua (assigned to Cairn Terrier), and two German Shorthaired Pointers (assigned to Kuvasz and Standard Poodle, respectively). All four errors involved breeds that did not form single-breed clusters in the structure analysis.

Having demonstrated that modern dog breeds form distinct genetic units, it was attempted to define broader historical relationships among the breeds. First, standard neighbor-joining methods were used to build a majority-rule consensus tree of breeds (FIG. **2**), with distances calculated using the chord distance measure (Cavalli-Sforza & Edwards (1967) *Evolution* 32:550), which does not assume a particular mutation model and is thought to perform well for closely related taxa (Goldstein et al. (1995) *Genetics* 139:463). The tree was rooted using wolf samples. The deepest split in the tree separated four Asian spitz-type breeds, and within this branch the Shar-Pei split first, followed by the Shiba Inu, with the Akita and Chow Chow grouping together. The second split separated the Basenji, an ancient African breed. The third split separated two Arctic spitz-type breeds, the Alaskan Malamute and Siberian Husky, and the fourth split separated two Middle Eastern sight hounds, the Afghan and Saluki, from the remaining breeds.

The first four splits exceeded the "majority rule" criterion, appearing in more than half of the bootstrap replicates. In contrast, the remaining breeds showed few consistent phylogenetic relationships, except for close groupings of five breed pairs that also clustered together in the structure analysis, one new pairing of the closely related West Highland White Terrier and Cairn Terrier, and the significant grouping of three Asian companion breeds of similar appearance, the Lhasa Apso, Shih Tzu, and Pekingese. A close relationship among these three breeds was also observed in the structure analysis, with at least two of the three clustering together in a majority of runs. The flat topology of the tree likely reflects a largely common founder stock and occurrence of extensive gene flow between phenotypically dissimilar dogs before the advent of breed clubs and breed barrier rules. In addition, it probably reflects the recreation of some historically older breeds that died out during the famines, depressions and wars of the 19th and 20th centuries, using stock from phenotypically similar or historically related dogs.

While the phylogenetic analysis showed separation of several breeds with ancient origins from a large group of breeds with presumed modern European origins, additional subgroups may be present within the latter group that are not detected by this approach for at least two reasons (Rosenberg et al. (2001) *Genetics* 159:699). First, the true evolutionary history of dog breeds is not well-represented by the bifurcating tree model assumed by the method, but rather involved mixing of existing breeds to create new breeds (a process that continues today). Second, methods based on genetic distance matrices lose information by collapsing all genotype data for pairs of breeds into a single number.

The clustering algorithm implemented in structure was explicitly designed to overcome these limitations (Pritchard et al. (2000) *Am. J. Hum. Genet.* 67:170-81; Falush et al. (2003) *Genetics* 164:1567; Rosenberg et al. (2001) *Genetics* 159:69-713) and has been applied to infer the genetic structure of several species (Rosenberg et al. (2002) *Science* 298: 2181-5; Falush et al. (2003) *Science* 299:1582-5; Rosenberg et al. (2001) *Genetics* 159:699-713). Structure was run on the entire data set using increasing values of K (the number of subpopulations the program attempts to find) to identify ancestral source populations. In this analysis, a modern breed could closely mirror a single ancestral population or represent a mixture of two or more ancestral types.

At K=2, one cluster was anchored by the first seven breeds to split in the phylogenetic analysis, while the other cluster contained the large number of breeds with a flat phylogenetic topology (Table 19A). Five runs of the program produced nearly identical results, with a similarity coefficient (Rosenberg et al. (2002) *Science* 298:2381) of 0.99 across runs. Seven other breeds share a sizeable fraction of their ancestry with the first cluster. These fourteen breeds all date to antiquity and trace their ancestry to Asia or Africa. When a diverse set of wolves from eight different countries was included in the analysis, they fell entirely within this cluster (Table 20). The branch leading to the wolf outgroup also fell within this group of breeds in the phylogenetic analysis (FIG. **2**).

At K=3, additional structure was detected that was not readily apparent from the phylogenetic tree (Table 19B). The new third cluster consisted primarily of breeds related in heritage and appearance to the Mastiff and is anchored by the Mastiff, Bulldog and Boxer, along with their close relatives the Bullmastiff, French Bulldog, Miniature Bull Terrier and Perro de Presa Canario. Also included in the cluster are the Rottweiler, Newfoundland and Bernese Mountain Dog, large breeds that are reported to have gained their size from ancient Mastiff-type ancestors. Less expected is the inclusion of the German Shepherd Dog. The exact origins of this breed are unknown, but the results suggest that the years spent as a military and police dog in the presence of working dog types, such as the Boxer, are responsible for shaping the genetic background of this popular breed. Three other breeds showed partial and inconsistent membership in this cluster across structure runs (Table 16), which lowered the similarity coefficient to 0.84.

At K=4, a fourth cluster was observed, which included several breeds used as herding dogs: Belgian Sheepdog, Belgian Tervuren, Collie and Shetland Sheepdog (Table 19C). The Irish Wolfhound, Greyhound, Borzoi and Saint Bernard were also frequently assigned to this cluster. While historical records do not suggest that these dogs were ever used to herd livestock, the results suggest that these breeds are either progenitors to, or descendants of, herding types. The breeds in the remaining cluster are primarily of relatively recent European origins, and are mainly different types of hunting dogs: scent hounds, terriers, spaniels, pointers and retrievers. Clustering at K=4 showed a similarity coefficient of 0.61, reflecting similar cluster membership assignments for most breeds but variable assignments for other breeds across runs (Table 16). At K=5 the similarity coefficient dropped to 0.26 and no additional consistent subpopulations were inferred, suggesting lack of additional high-level substructure in the sampled purebred dog population.

The results paint the following picture of the relationships among domestic dog breeds. Different breeds are genetically distinct, and individuals can be readily assigned to breeds based on their genotypes. This level of divergence is surprising given the short time since the origin of most breeds from mixed ancestral stocks and supports strong reproductive isolation within each breed as a result of the breed barrier rule. The results support at least four distinct breed groupings representing separate "adaptive radiations." A subset of breeds with ancient Asian and African origins splits off from the rest of the breeds and shows shared patterns of allele frequencies. At first glance, the inclusion of breeds from Central Africa (Basenji), the Middle East (Saluki and Afghan), as well as Tibet (Tibetan Terrier, Lhasa Apso), China (Chow Chow, Pekingese, Sharpei, Shi Tzu), Japan (Akita, Shiba Inu), and the Arctic (Alaskan Malamute, Siberian Husky, Samoyed) in a single genetic cluster is surprising. However, it is hypothesized that early pariah dogs originated in Asia and migrated with nomadic human groups both south to Africa and north to the Arctic, with subsequent migrations occurring throughout Asia (Savolainen et al. (2002) *Science* 298:1610; Leonard et al. (2002) *Science* 298:1613; Sablin & Khlopachev (2002) *Current Anthropology* 43:795). This cluster includes Nordic breeds that phenotypically resemble the wolf, such as the Alaskan Malamute and Siberian Husky, and shows the closest genetic relationship to the wolf, which is the direct ancestor of domestic dogs. Thus dogs from these breeds may be the best living representatives of the ancestral dog gene pool. It is notable that several breeds commonly believed to be of ancient origin are not included in this group, for example the Pharaoh Hound and Ibizan Hound. These are often thought to be the oldest of all dog breeds, descending directly from the ancient Egyptian dogs drawn on tomb walls more than 5000 years ago. The results indicate, however, that these two breeds have been recreated in more recent times from combinations of other breeds. Thus, while their appearance matches the ancient Egyptian sight hounds, their genomes do not. Similar conclusions apply to the Norwegian Elkhound, which clusters with modern European breeds rather than with the other Arctic dogs, despite reports of direct descent from Scandinavian origins over 5000 years ago (American Kennel Club (1998) *The Complete Dog Book*, eds. Crowley & Adelman, Howell Book House, New York, N.Y.; Wilcox & Walkowicz (1995) *Atlas of Dog Breeds of the World*, T.F.H. Publications, Neptune City, N.J.).

The large majority of breeds appears to represent a more recent radiation from shared European stock. While the individual breeds are genetically differentiated, they appear to have diverged at essentially the same time. This radiation probably reflects the proliferation of distinct breeds from less codified phenotypic varieties following the introduction of the breed concept and the creation of breed clubs in Europe in the 1800s. A more sensitive cluster analysis is able to discern additional genetic structure of three subpopulations within this group. One contains Mastiff-like breeds and appears to reflect shared morphology derived from a common ancestor. Another includes Shetland Sheep Dog, the two Belgian Sheepdogs, and Collie, and may reflect shared ancestral herding behavior. The remaining population is dominated by a proliferation of breeds dedicated to various aspects of the hunt. For these breeds, historical and breed club records suggest highly intertwined bloodlines, consistent with the results obtained.

Dog breeds have traditionally been grouped on the basis of their roles in human activities, physical phenotypes, and historical records. The results described above provide an independent classification based on patterns of genetic variation. This classification supports a subset of traditional groupings and also reveals previously unrecognized connections among breeds. An accurate understanding of the genetic relationships among breeds lays the foundation for studies aimed at uncovering the complex genetic basis of breed differences in morphology, behavior, and disease susceptibility.

Example 5

This example describes an in silico method for estimating the contribution of parent, grandparent and great-grandparent canids from different canid populations to the genomes of mixed progeny canids using microsatellite markers.

A. Methods

1. Dataset

Dataset 4 included genotype information for 95 markers from 85 canids, consisting of 81 dogs from 18 different dog breeds and 4 wolves (AHRT, AKIT, BEAG, BMD, BOX, BULD, BULM, CHIH, DACH, GOLD, IBIZ, MAST, NEWF, PEKE, POM, PRES, PUG, ROTT, WOLF, see Table 5 for abbreviations of canid populations). The 95 microsatellite markers were microsatellite markers 1-14, 16, 18-21, 23-36, 39-100 (Table 1). This dataset was chosen on the basis of the fact that greater than 90% of each of the 85 canids' genome was assigned to the correct breed. The four wolves were designated as one canid population. 12 breeds were represented by 5 dogs each, 3 breeds by 4 dogs, and 3 breeds by 3 dogs, as shown in Table 9. The genotypes for each of the microsatellite markers used in each canid are set forth in Table 3 (filed herewith on a compact disc).

2. Cluster Analyses

In silico canid mixes were created by randomly drawing one of the two alleles from each parent at each locus and designating them as the mix's alleles at that locus. An F1 mix was produced by an in silico mixing of alleles of two of the original 81 canids. An N2 mix was then produced by in silico mixing the F1 with one of its two parents, and an N3 mix was produced by in silico mixing the N2 with that same parent.

Three types of mixes were formed, test mixes, control mixes, and grandparent mixes. In the test mixes, the two parents were selected from two different breeds, chosen at random. 100 F1, N2, and N3 mixes were formed. Note that an F1 mix has two parents from different breeds, an N2 mix has three of four grandparents from one breed and one from another, and an N3 mix has seven of eight great-grandparents from one breed and one from another.

In the control mixes, the two parents were chosen from the same breed and 100 F1, N2, and N3 mixes were formed by the same procedure. Note that these all correspond to pure-bred dogs from the chosen breed.

Several grandparent mixes were also formed by choosing the four grandparents from 4 different breeds.

All the 300 test mixes were run together in a run of structure with the 85 chosen canids. The same analysis was performed for the control mixes, and for the 4 grandparent mixes. The program was run with the following parameter settings: #define NUMINDS 395; #define NUMLOCI 95; #define LABEL 1; #define POPDATA 1; #define POPFLAG 1; #define PHENOTYPE 0; #define MARKERNAMES 0; #define MAPDISTANCES 0; #define ONEROWPERIND 1; #define PHASEINFO 0; #define PHASED 0; #define EXTRACOLS 0; #define MISSING 0; #define PLOIDY 2; #define MAXPOPS 19; #define BURNIN 5000; #define NUMREPS 5000; #define USEPOPINFO 1; #define GENSBACK 0; #define MIGRPRIOR 0.0; #define NOADMIX 0; #define LINKAGE 0; #define INFERALPHA 1; #define ALPHA 1.0; #define POPALPHAS 0; #define UNIFPRIORALPHA 1; #define ALPHAMAX 10.0; #define ALPHAPROPSD 0.025; #define FREQSCORR 1; #define ONEFST 0; #define FPRIORMEAN 0.01; #define FPRIORSD 0.05; #define INFERLAMBDA 0; #define LAMBDA 1; #define COMPUTEPROB 1; #define PFROMPOPFLAGONLY 0; #define ANCESTDIST 1; #define NUMBOXES 1000; #define ANCESTPINT 0.95; #define STARTATPOPINFO 1; #define METROFREQ 10; #define UPDATEFREQ 1; #define PRINTQHAT 1.

Each of the 85 canids was designated as belonging to its appropriate breed, and the mixes were not assigned to any breed.

B. Results

For the control mixes, each mix was always assigned by the program to the correct breed, and the fraction of the genome assigned to that breed exceeded 95% in all 300 cases (the minimum was 95.75%), 98% in 297 cases, and 99% in 266 cases. Therefore, assignment of <95% of genome to a single breed provided unambiguous detection of mixing for the test mixes, and assignment of <98% provides strong evidence of mixing at the 0.99 confidence level.

For the F1 test mixes, all 100 mixes were correctly assigned genome contributions from the two parent breeds, with contributions of each breed ranging from 28% to 70%. In 82 of 100 cases each of the two parent breeds was assigned a contribution of >40% and <60%. This shows that mixes between two breeds can be reliably identified 100% of the time at the parent level.

For the N2 test mixes, 0.99 of 100 cases had <98% of the genome assigned to one breed, and 97 of 100 cases had <95% of the genome assigned to one breed, showing highly accurate ability to detect mixing at the grandparent level. In all but one case where mixing was detected, both breeds contributing to the mix were accurately identified (in one case the breed contributing one of the 4 grandparents was not detected as contributing significantly). In 80-85% of the cases, the N2 mixes could be reliably discriminated from F1 mixes (that is, it could be determined that the mixing occurred at the level of grandparents and not parents).

For the N3 test mixes, 85 of 100 cases had <98% of the genome assigned to one breed, and 77 of 100 cases had <95% of the genome assigned to one breed, showing fairly good ability to detect mixing at the great-grandparent level. In all cases where mixing was detected, both breeds contributing to the mix were accurately identified. In all cases, the N3 mixes could be reliably discriminated from F1 mixes (that is, it could be determined that the mixing occurred at the level of great-grandparents and not parents), but there was less ability to distinguish between mixes at the grandparent and great-grandparent levels.

Finally, for mixes with four different grandparents, all four grandparent breeds were reliably identified, with contributions of each breed to the genome of the mix estimated in the 20-30% range.

These results clearly demonstrate the ability of the method to discriminate mixes at the parent and grandparent level from pure-bred dogs (as well as ½ wolf and ¼ wolf mixes from dogs), with some ability to discriminate mixes at the great-grandparent level. The method also accurately identifies breed contributions in the genome of a mixed-breed dog. Larger databases containing more dogs from each breed, as well as additional markers and optimized sets of markers chosen according to criteria described elsewhere in this application, permits more accurate discrimination of mixing at the level of great-grandparents and, by straightforward extension, mixing that occurred in more distant ancestors.

Example 6

This example describes a representative method of the invention for estimating the contribution of canid populations to the genome of test canids using SNP markers.

A. Methods

1. Dataset

A dataset of single nucleotide polymorphisms (SNPs) in a variety of dog breeds was used to calculate the frequency of each allele in each breed. The database contained genotype information for 100 SNPs from 189 canids representing 67 breeds, with two to eleven purebred dogs per breed, as described in EXAMPLE 1. The identities of alleles in the dogs are set forth in Table 4 (filed herewith on a compact disc).

2. Doh Analysis

Using a leave-one-out procedure each dog was temporarily removed from the database and assigned to a breed based on comparison of the dog's genotypes to allele frequencies of each breed. Bayes' Theorem was used for the assignment: the probability that a dog comes from a given breed is the conditional probability that the observed genotype would occur in a dog of that breed divided by the sum of conditional probabilities that the observed genotype would occur for every breed in the database (essentially as described in Cornuet et al. (1999) *Genetics* 153:1989-2000). Software was developed to implement this algorithm. Breeds with only two individuals were included in the database but no attempt was made to classify their members because temporarily removing one of the two members did not leave enough information to calculate reliable allele frequencies.

B. Results

The output of this analysis was, for each dog, a list of the probabilities that the dog had come from each breed in the database, as shown in Table 21. Eighty percent of dogs were assigned to the correct breed with a probability of 99% or greater. For breeds in which genotypes were obtained for five or more individuals, 88% of the dogs were assigned to the correct breed with 99 percent probability. Fourteen dogs (sixteen percent of the total tested) were not assigned to the correct breed with better than 65% probability. Of these, thirteen were assigned incorrectly with a probability of fifty percent or better, nearly three-quarters with a probability of greater than ninety percent. The remaining dog was assigned 20-45% probabilities of coming from several breeds, one of which was correct.

These results demonstrate the feasibility of breed assignment based on SNP markers. Performance may be improved by generating SNP genotype profiles for a larger number of dogs (5 or more from each breed), using a larger set of SNPs, and selecting SNPs to be maximally informative. SNPs can be selected for inclusion in the panel both based on having a high heterozygosity across breeds (i.e., both alleles occur at high frequency) and based on large differences in frequency between breeds.

Example 7

This example describes a naive Bayesian classification model for estimating the contribution of parent and grandparent canids from different canid populations to the genomes of mixed progeny canids using microsatellite markers.

A. Methods

1. Dataset

Dataset 5 included genotype information for 96 markers from 429 canids representing 88 breeds (ACKR, AFGH, AHRT, AIRT, AKIT, AMAL, AMWS, ASBT, AUSS, AUST, BASS, BEAG, BEDT, BELS, BICH, BLDH, BMD, BORD, BORZ, BOX, BRIA, BSJI, BULD, BULM, CAIR, CHBR, CHIH, CHOW, CKCS, CLSP, COLL, DACH, DANE, DOBP, ECKR, FBLD, FCR, GOLD, GREY, GSD, GSHP, GSMD, GSNZ, HUSK, IBIZ, IRSE, IRTR, ITGR, IWOF, KEES, KERY, KOMO, KUVZ, LAB, LHSA, MAST, MBLT, MNTY, MSNZ, NELK, NEWF, OES, PEKE, PHAR, PNTR, POM, PRES, PTWD, PUG, RHOD, ROTT, SALU, SAMO, SCHP, SCWT, SHAR, SHIB, SHIH, SPOO, SSHP, SSNZ, STBD, TIBT, TERV, TPOO, WHIP, WHWT, WSSP, see Table 5 for abbreviations of canid populations). The 96 microsatellite markers were microsatellite markers 1-9, 11-38, 40-42, 44-75, 77-100 (Table 1). The genotype information for the canids in this dataset is set forth in Table 3 (filed herewith on a compact disc).

Dataset 6 included genotype information for 72 of the markers in Table 1 from 160 mixed-breed canids with known admixture composition. The genotype information for the mixed-breed canids in this dataset is set forth in Table 3 (filed herewith on a compact disc).

2. Analyses

A naïve Bayesian classification model was developed that incorporates linked and unlinked microsatellite loci information, higher-dimensioned ancestral populations, and higher-ordered generation pedigrees for the probabilistic assignment of individuals to mixtures of ancestral subpopulations. Two- and three-generational models were implemented for exact admixture detection and assignment, simultaneously addressing the generation, subpopulation and linkage limitations of previous models.

The 2-generational model closely follows the model outlined in Anderson & Thompson (2002) *Genetics* 160:1217-29, with extensions for greater than two classes of "pure" subpopulations. For the L unlinked loci, we have N subpopulations (deemed breeds), and j_l alleles at the l^{th} locus. For each individual at the L loci, we have a genotype: $(g_l^{(0)}, g_l^{(1)}$. Aggregating subpopulation allele information provides information about the frequency of any given allele, denoted as $f_{lj}^{(i)}$. Thus for individual, non-admixed subpopulation assignments we have:

$$P(g|\text{breed } i) = \prod_{l=1}^{L} f_{1g_l^{(0)}}^{(i)} f_{1g_l^{(1)}}^{(i)} \ \underline{\text{and}}\ P(\text{breed } i|g) = \frac{P(g|\text{breed } i)P(\text{breed } i)}{\sum_{i=1}^{N} P(g|\text{breed } i)P(\text{breed } i)}.$$

For a parental mixture assignment we now have:

$$P(g|b1 \text{ paternal, } b2 \text{ maternal}) = \prod_{l=1}^{L} \left\{ \left(f_{1g_l^{(0)}}^{(b_1)} f_{1g_l^{(1)}}^{(b_2)} + f_{1g_l^{(0)}}^{(b_2)} f_{1g_l^{(1)}}^{(b_1)} \right) I(g_l^{(0)} \neq g_l^{(1)}) + f_{1g_l}^{(b_1)} f_{1g_l}^{(b_2)} I(g_l^{(0)} = g_l^{(1)}) \right\}$$

where superscripts of (0) denote paternal relations and (1) denote maternal relations (with obvious interchangeability options).

The 3-generation model allows the extension of the model to consider 4-subpopulation, 2-generation representation across the N subpopulations:

$$P(g|(b1 \times b2) \times (b3 \times b4)) = \prod_{l=1}^{L} \left\{ \left[\left(.5f_{1g_l^{(0)}}^{(b_1)} + .5f_{1g_l^{(0)}}^{(b_2)} \right) \left(.5f_{1g_l^{(1)}}^{(b_3)} + .5f_{1g_l^{(1)}}^{(b_4)} \right) + \left(.5f_{1g_l^{(0)}}^{(b_1)} + .5f_{1g_l^{(1)}}^{(b_2)} \right) \right. \right.$$

-continued

$$\left. \left(.5f_{1g_l^{(1)}}^{(b_3)} + .5f_{1g_l^{(1)}}^{(b_4)} \right) \right] I(g_l^{(0)} \neq g_l^{(1)}) + \left. (.5f_{1g_l}^{(b_1)} + .5f_{1g_l}^{(b_2)})(.5f_{1g_l}^{(b_3)} + .5f_{1g_l}^{(b_4)}) I(g_l^{(0)} = g_l^{(1)}) \right\}$$

Exhaustive searches for the mixtures with the highest posterior probability are possible for 2- and 3-generation models.

For the in silico individuals, model validation was performed via a leave-one-out cross validation, where sampled alleles used in creating the in silico mixed-breed individual are removed from the ancestral population and allele frequencies are updated prior to maximum likelihood mixture proportion assignment.

B. Results

Analysis on in-silico mixed-breed individuals across all 96 dinucleotide markers show that the model at 2- and 3-generations performs exceedingly well with 98.4% of F1 mixes and 94.3% of F2 mixes correctly assigned, with no obvious patterns for breed-specific deficits. Analysis on the 160 known mixed-breed individuals genotyped at 72 of the 96 dinucleotide markers show that the model at 2- and 3-generations performs nearly as accurately with 96.2% of F1 mixes and 91.8% of F2 mixes correctly assigned.

While the preferred embodiment of the invention has been illustrated and described, it will be appreciated that various changes can be made therein without departing from the spirit and scope of the invention.

TABLE 1

Microsatellite Markers

	Marker Name	Forward Primer	Reverse Primer	Reference	Ann. Temp. (° C.)	PIC
1	REN285G14	SEQ ID NO: 1	SEQ ID NO: 101	1[a]	55	NA
2	C01.673	SEQ ID NO: 2	SEQ ID NO: 102	1	58	0.36
3	REN112I02	SEQ ID NO: 3	SEQ ID NO: 103	1	58	0.76
4	REN172C02	SEQ ID NO: 4	SEQ ID NO: 104	1	55	0.48
5	FH2793	SEQ ID NO: 5	SEQ ID NO: 105	2[b]	58	0.76
6	REN143K19	SEQ ID NO: 6	SEQ ID NO: 106	1	55	0.5
7	FH2890	SEQ ID NO: 7	SEQ ID NO: 107	2	55	0.59
8	C02.466	SEQ ID NO: 8	SEQ ID NO: 108	1	58	0.55
9	C02.894	SEQ ID NO: 9	SEQ ID NO: 109	1	58	0.72
10	C02.342	SEQ ID NO: 10	SEQ ID NO: 110	1		0.77
11	FH2895	SEQ ID NO: 11	SEQ ID NO: 111	2	58	0.7
12	REN157C08	SEQ ID NO: 12	SEQ ID NO: 112	1	55	0.72
13	C03.445	SEQ ID NO: 13	SEQ ID NO: 113	1	58	0.6
14	FH2732	SEQ ID NO: 14	SEQ ID NO: 114	2	58	0.84
15	FH2776	SEQ ID NO: 15	SEQ ID NO: 115	2	58	0.49
16	REN160J02	SEQ ID NO: 16	SEQ ID NO: 116	1	58	0.82
17	REN262N08	SEQ ID NO: 17	SEQ ID NO: 117	1	55	0.72
18	REN92G21	SEQ ID NO: 18	SEQ ID NO: 118	1	58	0.66
19	REN285I23	SEQ ID NO: 19	SEQ ID NO: 119	1	55	0.58
20	C05.414	SEQ ID NO: 20	SEQ ID NO: 120	1	58	0.47
21	FH2752	SEQ ID NO: 21	SEQ ID NO: 121	2	58	0.38
22	REN210I14	SEQ ID NO: 22	SEQ ID NO: 122	1	55	0.66
23	REN37H09	SEQ ID NO: 23	SEQ ID NO: 123	3[c]	58	0.67
24	REN97M11	SEQ ID NO: 24	SEQ ID NO: 124	1	55	NA
25	REN286L19	SEQ ID NO: 25	SEQ ID NO: 125	1	58	0.66
26	FH2860	SEQ ID NO: 26	SEQ ID NO: 126	2	55	0.62
27	REN204K13	SEQ ID NO: 27	SEQ ID NO: 127	1	55	0.48
28	C08.373	SEQ ID NO: 28	SEQ ID NO: 128	1	58	0.68
29	C08.618	SEQ ID NO: 29	SEQ ID NO: 129	1	55	0.82
30	C09.173	SEQ ID NO: 30	SEQ ID NO: 130	1	58	0.78
31	C09.474	SEQ ID NO: 31	SEQ ID NO: 131	1	55	0.78
32	FH2885	SEQ ID NO: 32	SEQ ID NO: 132	2	55	0.74
33	C10.781	SEQ ID NO: 33	SEQ ID NO: 133	1	55	0.62

TABLE 1-continued

Microsatellite Markers

	Marker Name	Forward Primer	Reverse Primer	Reference	Ann. Temp. (° C.)	PIC
34	REN73F08	SEQ ID NO: 34	SEQ ID NO: 134	1	55	0.54
35	REN154G10	SEQ ID NO: 35	SEQ ID NO: 135	1	55	0.71
36	REN164B05	SEQ ID NO: 36	SEQ ID NO: 136	1	55	0.5
37	FH2874	SEQ ID NO: 37	SEQ ID NO: 137	2	55	NA
38	C11.873	SEQ ID NO: 38	SEQ ID NO: 138	1	58	0.81
39	REN258L11	SEQ ID NO: 39	SEQ ID NO: 139	1		0.72
40	REN213F01	SEQ ID NO: 40	SEQ ID NO: 140	1	55	0.82
41	REN208M20	SEQ ID NO: 41	SEQ ID NO: 141	1	58	0.64
42	REN94K11	SEQ ID NO: 42	SEQ ID NO: 142	1	55	0.56
43	REN120P21	SEQ ID NO: 43	SEQ ID NO: 143	1		0.5
44	REN286P03	SEQ ID NO: 44	SEQ ID NO: 144	1	58	0.78
45	C13.758	SEQ ID NO: 45	SEQ ID NO: 145	1	55	0.75
46	C14.866	SEQ ID NO: 46	SEQ ID NO: 146	1	55	0.74
47	FH3072	SEQ ID NO: 47	SEQ ID NO: 147	2	55	0.63
48	FH3802	SEQ ID NO: 48	SEQ ID NO: 148	2	55	0.44
49	REN06C11	SEQ ID NO: 49	SEQ ID NO: 149	3	58	0.79
50	REN144M10	SEQ ID NO: 50	SEQ ID NO: 150	1	58	0.66
51	REN85N14	SEQ ID NO: 51	SEQ ID NO: 151	1	58	0.78
52	FH3096	SEQ ID NO: 52	SEQ ID NO: 152	2	55	0.79
53	C17.402	SEQ ID NO: 53	SEQ ID NO: 153	1	58	0.75
54	REN50B03	SEQ ID NO: 54	SEQ ID NO: 154	3	58	0.74
55	REN112G10	SEQ ID NO: 55	SEQ ID NO: 155	1	55	0.7
56	REN186N13	SEQ ID NO: 56	SEQ ID NO: 156	1	58	0.66
57	FH2795	SEQ ID NO: 57	SEQ ID NO: 157	2	58	0.71
58	C18.460	SEQ ID NO: 58	SEQ ID NO: 158	1	58	0.53
59	FH2783	SEQ ID NO: 59	SEQ ID NO: 159	2	55	NA
60	REN91I14	SEQ ID NO: 60	SEQ ID NO: 160	1	58	0.72
61	REN274F18	SEQ ID NO: 61	SEQ ID NO: 161	1	58	0.66
62	FH2887	SEQ ID NO: 62	SEQ ID NO: 162	2	55	0.77
63	FH3109	SEQ ID NO: 63	SEQ ID NO: 163	2	58	0.62
64	REN293N22	SEQ ID NO: 64	SEQ ID NO: 164	1	58	0.48
65	FH2914	SEQ ID NO: 65	SEQ ID NO: 165	2	55	0.61
66	FH3069	SEQ ID NO: 66	SEQ ID NO: 166	2	55	0.53
67	REN49F22	SEQ ID NO: 67	SEQ ID NO: 167	3	55	0.66
68	REN107H05	SEQ ID NO: 68	SEQ ID NO: 168	1	55	0.86
69	REN78I16	SEQ ID NO: 69	SEQ ID NO: 169	1	55	0.63
70	FH3078	SEQ ID NO: 70	SEQ ID NO: 170	2	55	0.67
71	C23.277	SEQ ID NO: 71	SEQ ID NO: 171	1	55	0.54
72	REN181K04	SEQ ID NO: 72	SEQ ID NO: 172	1	58	0.64
73	REN106I06	SEQ ID NO: 73	SEQ ID NO: 173	1	55	0.58
74	FH3083	SEQ ID NO: 74	SEQ ID NO: 174	2	55	0.61
75	REN54E19	SEQ ID NO: 75	SEQ ID NO: 175	1	55	0.54
76	C25.213	SEQ ID NO: 76	SEQ ID NO: 176	1		0.78
77	REN87O21	SEQ ID NO: 77	SEQ ID NO: 177	1	55	0.62
78	C26.733	SEQ ID NO: 78	SEQ ID NO: 178	1	55	0.61
79	C27.442	SEQ ID NO: 79	SEQ ID NO: 179	1	55	0.74
80	C27.436	SEQ ID NO: 80	SEQ ID NO: 180	1	55	0.51
81	REN72K15	SEQ ID NO: 81	SEQ ID NO: 181	1	55	0.66
82	FH2759	SEQ ID NO: 82	SEQ ID NO: 182	2	55	0.71
83	FH2785	SEQ ID NO: 83	SEQ ID NO: 183	2	55	0.46
84	REN239K24	SEQ ID NO: 84	SEQ ID NO: 184	1	55	0.78
85	FH3082	SEQ ID NO: 85	SEQ ID NO: 185	2	55	0.54
86	REN51C16	SEQ ID NO: 86	SEQ ID NO: 186	4[d]	55	0.8
87	FH3053	SEQ ID NO: 87	SEQ ID NO: 187	2	55	0.74
88	REN43H24	SEQ ID NO: 88	SEQ ID NO: 188	3	55	0.66
89	FH2712	SEQ ID NO: 89	SEQ ID NO: 189	2	55	0.67
90	FH2875	SEQ ID NO: 90	SEQ ID NO: 190	2	55	0.6
91	FH2790	SEQ ID NO: 91	SEQ ID NO: 190	2	55	0.58
92	REN291M20	SEQ ID NO: 92	SEQ ID NO: 192	1	58	0.76
93	REN160M18	SEQ ID NO: 93	SEQ ID NO: 193	1	58	0.76
94	FH3060	SEQ ID NO: 94	SEQ ID NO: 194	2	55	0.4
95	REN314H10	SEQ ID NO: 95	SEQ ID NO: 195	1	55	0.54
96	REN01G01	SEQ ID NO: 96	SEQ ID NO: 196	3	55	0.54
97	REN112C08	SEQ ID NO: 97	SEQ ID NO: 197	1	55	0.42
98	REN106I07	SEQ ID NO: 98	SEQ ID NO: 198	1	55	0.78
99	FH2708	SEQ ID NO: 99	SEQ ID NO: 199	2	55	0.63
100	REN86G15	SEQ ID NO: 100	SEQ ID NO: 200	1	55	0.76

[a] Breen et al. (2001) Genome Res. 11: 1784–95.
[b] Guyon et al. (2003) Proc. Natl. Acad. Sci. U.S.A. 100(9): 5296–301.
[c] Jouquand et al. (2000) Animal Genetics 31: 266–72.
[d] Mellersh et al. (2000) Mamm. Genome 11: 120–30.

TABLE 2

SNP Markers

BAC	Forward Primer	Reverse Primer	SNP*	Major Allele	Minor Allele	Minor Allele Frequency**	Heterozygosity**
372-c5t (SEQ ID NO: 202)	SEQ ID NO: 244	SEQ ID NO: 286	82	C	T	0.004	0.009
			133	T	C	ND	ND
372-c15t (SEQ ID NO: 203)	SEQ ID NO: 245	SEQ ID NO: 287	285	G	A	0.013	0.025
372-e2s (SEQ ID NO: 204)	SEQ ID NO: 246	SEQ ID NO: 288	271	G	T	0.029	0.057
			257	C	T	0.071	0.132
			128	C	G	0.046	0.087
			93	C	G	0.021	0.041
			50	A	—	ND	ND
372-e13t (SEQ ID NO: 205)	SEQ ID NO: 247	SEQ ID NO: 289	57	T	C	0.004	0.008
372-e15t(SEQ ID NO: 206)	SEQ ID NO: 248	SEQ ID NO: 290	312	—	A	ND	ND
			301	C	T	ND	ND
			258	C	T	0.009	0.018
			156	—	T	ND	ND
372-e16s (SEQ ID NO: 207)	SEQ ID NO: 249	SEQ ID NO: 291	254	G	A	ND	ND
372-e18t (SEQ ID NO: 208)	SEQ ID NO: 250	SEQ ID NO: 292	165	G	C	0.254	0.379
372-g17t (SEQ ID NO: 209)	SEQ ID NO: 251	SEQ ID NO: 293	66	T	A	0.134	0.232
372-i23s (SEQ ID NO: 210)	SEQ ID NO: 252	SEQ ID NO: 294	384	A	G	0.312	0.429
372-m6t (SEQ ID NO: 211)	SEQ ID NO: 253	SEQ ID NO: 295	138	C	A	0.275	0.399
			88	T	C	0.004	0.009
			266	T	G	ND	ND
372-m7s (SEQ ID NO: 212)	SEQ ID NO: 254	SEQ ID NO: 296	317	T	A	ND	ND
372-m9t (SEQ ID NO: 213)	SEQ ID NO: 255	SEQ ID NO: 297	108	A	T	0.368	0.465
			58	G	C	0.362	0.462
372-m18t (SEQ ID NO: 214)	SEQ ID NO: 256	SEQ ID NO: 298	170	—	T	ND	ND
			129	G	A	0.159	0.267
372-m23t (SEQ ID NO: 215)	SEQ ID NO: 257	SEQ ID NO: 299	76	C	T	0.017	0.034
			108	G	A	0.081	0.149
			229	G	A	0.078	0.143
			238	T	C	0.078	0.143
			263	A	G	0.157	0.265
372-o13s (SEQ ID NO: 216)	SEQ ID NO: 258	SEQ ID NO: 300	212	T	C	0.316	0.433
373-a10s (SEQ ID NO: 217)	SEQ ID NO: 259	SEQ ID NO: 301	274	T	C	0.131	0.228
373-a15t (SEQ ID NO: 218)	SEQ ID NO: 260	SEQ ID NO: 302	112	G	A	0.004	0.008
373-a17t (SEQ ID NO: 219)	SEQ ID NO: 261	SEQ ID NO: 303	73	G	A	ND	ND
			136	A	G	0.394	0.477
373-a21s (SEQ ID NO: 220)	SEQ ID NO: 262	SEQ ID NO: 304	89	C	T	0.017	0.034
373-c13s (SEQ ID NO: 221)	SEQ ID NO: 263	SEQ ID NO: 305	93	C	T	0.028	0.054
373-c15t (SEQ ID NO: 222)	SEQ ID NO: 264	SEQ ID NO: 306	242	C	T	0.209	0.331
			202	C	T	0.174	0.288
			131	—	AA	ND	ND
373-e1t (SEQ ID NO: 223)	SEQ ID NO: 265	SEQ ID NO: 307	50	T	C	0.009	0.019
			102		Del. 8 bp	ND	ND
			130	G	A	0.01	0.02
373-e21t (SEQ ID NO: 224)	SEQ ID NO: 266	SEQ ID NO: 308	282	A	G	0.049	0.093
			116	C	T	0.215	0.338
373-g7t (SEQ ID NO: 225)	SEQ ID NO: 267	SEQ ID NO: 309	243	C	T	0.014	0.028
			242	G	A	ND	ND
			84	T	—	ND	ND
373-g19t (SEQ ID NO: 226)	SEQ ID NO: 268	SEQ ID NO: 310	249	—	A	ND	ND
			251	A	—	ND	ND
			246	G	A	0.004	0.008
			224	T	C	ND	ND
			378	A	C	0.082	0.15
373-i8s (SEQ ID NO: 227)	SEQ ID NO: 269	SEQ ID NO: 311	199	A	C	0.073	0.136
			224	G	A	0.004	0.009
373-i16s (SEQ ID NO: 228)	SEQ ID NO: 270	SEQ ID NO: 312	312	A	G	0.078	0.144
			254	G	A	0.24	0.365
			250	C	T	0.079	0.146
			249	C	T	0.031	0.06
373-k8s (SEQ ID NO: 229)	SEQ ID NO: 271	SEQ ID NO: 313	181	C	T	0.005	0.009
			224		Del. 2 bp	ND	ND
373-k10t (SEQ ID NO: 230)	SEQ ID NO: 272	SEQ ID NO: 314	261	A	C	0.353	0.457
			264	T	C	0.008	0.017
372-c5s (SEQ ID NO: 231)	SEQ ID NO: 273	SEQ ID NO: 315	112	A	G	0.357	0.459
			168	A	G	0.01	0.02
372-c15s (SEQ ID NO: 232)	SEQ ID NO: 274	SEQ ID NO: 316	121	T	C	0.017	0.034
			196	G	A	0.004	0.009
372-e15s (SEQ ID NO: 233)	SEQ ID NO: 275	SEQ ID NO: 317	67	A	G	0.186	0.303
			71	A	C	0.013	0.026
			165	G	A	0.105	0.188
			221	C	A	0.189	0.307
372-i23t (SEQ ID NO: 234)	SEQ ID NO: 276	SEQ ID NO: 318	97	A	G	0.119	0.21
			224	—	T	ND	ND

TABLE 2-continued

SNP Markers

BAC	Forward Primer	Reverse Primer	SNP*	Major Allele	Minor Allele	Minor Allele Frequency**	Heterozygosity**
372-m6s (SEQ ID NO: 235)	SEQ ID NO: 277	SEQ ID NO: 319	67	A	G	0.323	0.437
			73	A	C	0.042	0.081
			100	T	C	0.042	0.081
			108	C	T	ND	ND
			127	T	A	ND	ND
			147	T	G	0.349	0.454
			186	A	G	0.008	0.017
372-m7t (SEQ ID NO: 236)	SEQ ID NO: 278	SEQ ID NO: 320	100	C	A	0.101	0.181
			273	A	G	0.051	0.097
372-m18s (SEQ ID NO: 237)	SEQ ID NO: 279	SEQ ID NO: 321	131	T	C	0.339	0.448
373-a14t (SEQ ID NO: 238)	SEQ ID NO: 280	SEQ ID NO: 322	290	T	C	0.224	0.347
			197	C	T	0.225	0.349
			160	A	T	0.441	0.493
			55	T	—	ND	ND
373-a21t (SEQ ID NO: 239)	SEQ ID NO: 281	SEQ ID NO: 323	93	A	G	0.008	0.017
373-e21s (SEQ ID NO: 240)	SEQ ID NO: 282	SEQ ID NO: 324	136	C	T	0.332	0.443
			175	C	T	0.332	0.443
			191	G	C	0.33	0.442
373-g7s (SEQ ID NO: 241)	SEQ ID NO: 283	SEQ ID NO: 325	263	C	T	0.204	0.325
			266	T	C	0.201	0.321
373-i16t (SEQ ID NO: 242)	SEQ ID NO: 284	SEQ ID NO: 326	47	G	A	0.457	0.496
			133	C	T	ND	ND
			173	G	A	ND	ND
			210	G	A	ND	ND
			302	C	T	0.476	0.499
			319	C	A	0.381	0.472
373-k16t (SEQ ID NO: 243)	SEQ ID NO: 285	SEQ ID NO: 327	54	—	A	ND	ND

*Position from 5' Forward Primer.
**Based on 120 canids representing 60 breeds.
ND = Not done.

TABLE 5

Abbreviations for Canid Populations

ACKR	American Cocker Spaniel
AFGH	Afghan Hound
AHRT	American Hairless Terrier
AIRT	Airedale Terrier
AKAB	Akabash
AKIT	Akita
AMAL	Alaskan Malamute
AMWS	American Water Spaniel
ASBT	American Staffordshire Bull Terrier
AUSS	Australian Shepherd
AUST	Australian Terrier
BASS	Basset Hound
BEAC	Bearded Collie
BEAG	Beagle
BEDT	Bedlington Terrier
BELS	Belgian Sheepdog
BICH	Bichon Frise
BLDH	Bloodhound
BMD	Bernese Mountain Dog
BORD	Border Collie
BORZ	Borzoi
BOST	Boston Terrier
BOX	Boxer
BOYK	Boykin Spaniel
BRIA	Briard
BSJI	Basenji
BULD	Bulldog
BULM	Bullmastiff
BULT	Bull Terrier
CAIR	Cairn Terrier
CHBR	Chesapeak Bay Retriever
CHIH	Chihuahua
CHOW	Chow Chow
CKCS	Cavalier King Charles Spaniel
CLSP	Clumber Spaniel

TABLE 5-continued

Abbreviations for Canid Populations

COLL	Collie
COY	Coyote
DACH	Dachshund
DALM	Dalmatian
DANE	Great Dane
DNDT	Dandie Dinmont Terrier
DOBP	Doberman Pinscher
ECKR	English Cocker Spaniel
ESHP	English Shepherd
ESPR	English Springer Spaniel
EFOX	English Foxhound
FCR	Flat-Coated Retriever
FBLD	French Bulldog
FSP	Field Spaniel
GOLD	Golden Retriever
GREY	Greyhound
GPIN	German Pincher
GSD	German Shepherd Dog
GSHP	German Short-haired Pointer
GSMD	Greater Swiss Mountain Dog
GSNZ	Giant Schnauzer
HUSK	Siberian Husky
IBIZ	Ibizan Hound
IRSE	Irish Setter
IRTR	Irish Terrier
IRWS	Irish Water Spaniel
IWOF	Irish Wolfhound
ITGR	Italian Greyhound
KEES	Keeshond
KERY	Kerry Blue Terrier
KOMO	Komondor
KUVZ	Kuvasz
LAB	Labrador Retriever
LHSA	Lhasa Apso
MAST	Mastiff

TABLE 5-continued

Abbreviations for Canid Populations	
MBLT	Miniature Bull Terrier
MNTY	Manchester Terrier - toy
MSNZ	Miniature Schnauzer
NELK	Norwegian Elkhound
NEWF	Newfoundland
OES	Old English Sheepdog
PAPI	Papillon
PEKE	Pekingese
PBGV	Petit Basset Griffon Vendeen
PHAR	Pharaoh Hound
PNTR	Pointer
POM	Pomeranian
PRES	Presa Canario
PTWD	Portuguese Water Dog
PUG	Pug
RHOD	Rhodesian Ridgeback
ROTT	Rottweiler
SALU	Saluki
SAMO	Samoyed
SCHP	Schiperke
SCDH	Scottish Deerhound
SCWT	Soft-coated Wheaten Terrier
SFXT	Smooth Fox Terrier
SHAR	Shar-Pei
SHIB	Shiba Ina
SHIH	Shih Tzu
SPIN	Spinoni Italiano
SPIX	Springer Mix
SCOL	Standard Collie
SPOO	Standard Poodle
SSNZ	Standard Schnauzer
SSHP	Shetland Sheepdog
STBD	Saint Bernard
SUSP	Sussex Spaniel
TERV	Belgian Tervuren
TIBT	Tibetan Terrier
TPOO	Toy Poodle
WEIM	Weimaraner
WHIP	Whippet
WHWT	West Highland White Terrier
WOLF	Wolf
WSSP	Welsh Springer Spaniel
WST	Welsh Terrier

TABLE 6

94 Canids in Dataset 1

Population*	Canid Identification Number				
AHRT	1120	1121	1122	1123	1124
AKIT	1130	1131	1132	1133	1134
BEAG	994	995	1323	1324	1327
BMD	941	943	968	970	971
BOX	1176	1177	1178	1179	1304
BULD	1193	1194	1195	1197	1198
BULM	1105	1106	1107	1108	1109
CHIH	1202	1203	1204	1205	1206
DACH	1051	1052	1053	1054	1055
GOLD	591	592	593	603	604
IBIZ	1147	1148	1162	1172	1280
MAST	991	1015	1016	1017	1066
NEWF	271	274	275	277	278
PEKE	1143	1145	1211	1212	1213
POM	1190	1191	1210	1238	1239
PRES	1082	1093	1096	1115	1127
PUG	1077	1104	1183	1184	1192
ROTT	1014	1028	1019	1033	1034
WOLF	282135	492-8	930121	Iran-1	

*See Table 5 for abbreviations of canid populations.

TABLE 7

341 Canids in Dataset 2

Population*	Canid Identification Number					
ACKR	1035	2261	2310			
AFGH	1812	1939	2264			
AHRT	1120	1121	1122	1123	1124	
AIRT	1603	1604	1788	1875		
AKIT	1130	1131	1132	1133	1134	
AMAL	1629	1779	1845	2132	2214	
AMWS	2168	2279	2327	987	988	
AUSS	1336	1337	1500	1521	1683	
AUST	1387	1531	1533	1564	1870	1871
BASS	1341	1342	1506	1917		
BEAG	1323	1324	1327	994	995	
BEDT	1422	1423	1424	1426		
BELS	1351	2111	2153	2209	2210	
BLDH	1186	1223	1410	1942	1957	
BMD	941	943	968	1763	969	
BORD	1648	1828	1829	2002	2003	
BORZ	1378	1401	1808	2268	978	
BOX	1176	1177	1178	1179	1304	
BSJI	1338	1339	1645	1675	1717	
BULD	1193	1194	1195	1197	1198	
BULM	1105	1106	1107	1108	1109	
CAIR	1405	2096	2113	2125	2131	
CHBR	1546	1549	1813	2091	888	
CHIH	1202	1203	1204	1205	1206	
CKCS	1513	1639	1640	1642	2054	
CLSP	1008	1009	1802	2312	2314	
COLL	1692	1701	2284	373	379	
DACH	1051	1052	1053	1054	1055	
DANE	1574	1575	1580	1700	1748	
DNDT	2204	2219	2221			
DOBP	1031	1749	2162	2245		
ECKR	1376	1377	1400	1404	1511	
FCR	1188	2020	2042	2044	2259	
GOLD	591	592	593	603	604	
GREY	2277	2478	2479	2480	2481	
GSD	1666	1776	2011	2060	2086	
GSHP	1628	1708	1710	1833	1892	
GSMD	1547	1659	1660	1662	1663	
HUSK	1469	1883	2115	2117	2118	
IBIZ	1147	1148	1162	1172	1280	
IRSE	1540	1617	1896	2084	2085	
IRTR	2152	2189	2238	2242		
IWOF	1581	1761	1792	1906	1993	
KEES	1501	1589	1818	1819	2072	
KOMO	1484	1964	2321	2323	2334	
KUVZ	1482	1551	1672	1913	1994	
LAB	1310	1465	1468	1754	1830	
MAST	1015	1016	1017	1066	991	
MBLT	1915	2253	2254	2255	2256	
MNTY	1539	1732	2145	2149		
NELK	2216	2239	2240	2281	2295	
NEWF	271	274	275	277	278	
OES	1984	2171	2179			
PEKE	1143	1145	1211	1212	1213	
PNTR	1382	1383	1869	1938	1948	
POM	1190	1191	1210	1238	1239	
PRES	1082	1096	1115	1127	1095	
PTWD	P142	P1	P238	P25	P67	
PUG	1077	1104	1183	1184	1192	
RHOD	1444	1454	1505	1592	1609	
ROTT	1014	1028	1029	1033	1034	
SCHP	1386	1471	1814	1852		
SCWT	1624	1770	2250	2301		
SFXT	1550	2167				
SHAR	1573	1593	1619	1998	1999	
SPOO	1530	1582	1876	1877	2337	
SSHP	1379	1523	1824	1921	2040	
STBD	1075	1714	1750	2403	2404	
TERV	1622	2194	2200	2222		
WHIP	1355	1395	1407	1409	1518	
WHWT	1388	1420	1992	2100	2128	
WSSP	1955	2139	2143	2195	2286	

*See Table 5 for abbreviations of canid populations.

TABLE 8

414 Canids in Dataset 3

Population*	Canid Identification Number				
ACKR	1035	2261	2310	1956	2260
AFGH	1812	1939	2264	1936	1937
AHRT	1120	1121	1122	1123	1124
AIRT	1603	1604	1788	1875	
AKIT	1130	1131	1132	1133	1134
AMAL	1629	1779	1845	2132	2214
AMWS	2168	2279	2327	987	988
AUSS	1336	1337	1500	1521	1683
AUST	1387	1531	1564	1870	1871
BASS	1341	1342	1506	1917	
BEAG	1323	1324	1327	994	995
BEDT	1422	1423	1424	1426	
BELS	1351	2111	2153	2209	2210
BICH	1943	1954	933	974	
BLDH	1186	1223	1410	1942	1957
BMD	941	943	968	1763	969
BORD	1648	1828	1829	2002	2003
BORZ	1378	1401	1808	2268	978
BOX	1176	1177	1178	1179	1304
BSJI	1338	1339	1645	1675	1717
BULD	1193	1194	1195	1197	1198
BULM	1105	1106	1107	1108	1109
CAIR	1405	2096	2113	2125	2131
CHBR	1546	1549	1813	2091	888
CHIH	1202	1203	1204	1205	1206
CHOW	1633	1835	1837	1838	1839
CKCS	1513	1639	1640	1642	2054
CLSP	1008	1009	1802	2312	2314
COLL	1692	1701	2284	373	379
DACH	1051	1052	1053	1054	1055
DANE	1574	1575	1580	1700	1748
DOBP	1031	1032	1749	2162	2245
ECKR	1376	1377	1400	1404	1511
FBLD	1507	1508	1509	2671	
FCR	1188	2020	2042	2044	2259
GOLD	591	592	593	603	604
GREY	2477	2478	2479	2480	2481
GSD	1666	1776	2011	2060	2086
GSHP	1628	1708	1710	1833	1892
GSMD	1547	1659	1660	1662	1663
GSNZ	1868	22739	27093	27106	33390
HUSK	1469	1883	2115	2117	2118
IBIZ	1147	1148	1162	1172	1280
IRSE	1540	1617	1896	2084	2085
IRTR	2152	2189	2238	2242	
ITGR	1568	1570	1862	1881	1882
IWOF	1581	1761	1792	1906	1993
KEES	1501	1589	1818	1819	2072
KERY	13878	1483	1579	2014	24255
KOMO	1484	1964	2321	2323	2334
KUVZ	1482	1551	1672	1913	1994
LAB	1310	1465	1468	1754	1830
LHSA	1524	1525	1526	1528	2074
MAST	1015	1016	1017	1066	991
MBLT	1915	2253	2254	2255	2256
MNTY	1539	1732	2145	2149	
MSNZ	1587	1756	1851	2034	2613
NELK	2216	2239	2240	2281	2295
NEWF	271	274	275	277	278
OES	1984	2171	2179	1914	1626
PEKE	1143	1145	1211	1212	1213
PHAR	1292	1947	1962	1963	
PNTR	1382	1383	1869	1938	1948
POM	1190	1191	1210	1238	1239
PRES	1082	1096	1115	1127	1095
PTWD	P142	P1	P238	P25	P67
PUG	1077	1104	1183	1184	1192
RHOD	1444	1454	1505	1592	1609
ROTT	1014	1028	1029	1033	1034
SALU	1491	1535	1607	1873	2610
SAMO	1375	1532	1560	169	239
SCHP	1386	1471	1814	1852	
SCWT	1624	1770	2250	2301	
SHAR	1573	1593	1619	1998	1999
SHIB	1769	1854	1856	1860	1981
SHIH	1393	1783	2068	2859	2860
SPOO	1530	1582	1876	1877	2337
SSHP	1379	1523	1824	1921	2040
SSNZ	13352	1360	1827	20457	22647
STBD	1075	1714	1750	2403	2404
TIBT	1466	1562	1707	26078	28086
TERV	1622	2194	2200	2222	
WHIP	1355	1395	1407	1409	1518
WHWT	1388	1420	1992	2100	2128
WSSP	1955	2139	2143	2195	2286

*See Table 5 for abbreviations of canid populations.

TABLE 9

85 Canids in Dataset 5

Population*	Canid Identification Number				
AHRT	1120	1121	1124		
AKIT	1130	1131	1132	1133	1134
BEAG	1323	1327	994	995	
BMD	941	943	968	970	971
BOX	1176	1177	1178	1179	1304
BULD	1193	1194	1195	1197	1198
BULM	1105	1106	1107	1108	1109
CHIH	1202	1203	1204		
DACH	1051	1052	1053	1054	1055
GOLD	591	593	603	604	
IBIZ	1147	1148	1162	1172	1280
MAST	1015	1016	1017	1066	991
NEWF	271	274	275	277	278
PEKE	1143	1145	1211	1212	1213
POM	1190	1191	1210	1238	
PRES	1093	1096	1115		
PUG	1077	1104	1183	1184	1192
ROTT	1014	1028	1029	1033	1034
WOLF	282135	492-8	930121	Iran-1	

*See Table 5 for abbreviations of canid populations.

TABLE 10

Microsatellite Marker Alleles and Heterozygosities in 19 Canid Populations

Population*	n	P	A	Ap	He	Ho	f
AHRT	4.882353	0.835294	2.576471	2.887324	0.439286	0.432549	0.017577
AKIT	4.8	0.917647	3.035294	3.217949	0.550509	0.522157	0.058242
BEAG	4.941176	0.929412	2.952941	3.101266	0.560938	0.482941	0.153823
BMD	3.938272	0.82716	2.296296	2.552239	0.396752	0.38642	0.095341
BOX	4.905882	0.764706	2.141176	2.492308	0.348287	0.308235	0.13062
BULD	4.8	0.870588	2.6	2.837838	0.47183	0.42902	0.104385

TABLE 10-continued

Microsatellite Marker Alleles and Heterozygosities in 19 Canid Populations

Population*	n	P	A	Ap	He	Ho	f
BULM	4.952941	0.917647	2.752941	2.910256	0.518151	0.488235	0.064621
CHIH	4.811765	0.976471	3.447059	3.506024	0.611858	0.556667	0.101951
DACH	4.847059	0.882353	2.658824	2.853333	0.487712	0.482941	0.016864
GOLD	4.905882	0.905882	2.905882	3.103896	0.529542	0.520784	0.018744
IBIZ	4.682353	0.905882	2.847059	3.038961	0.517372	0.462745	0.118169
MAST	4.576471	0.905882	2.541176	2.701299	0.488389	0.466667	0.051889
NEWF	4.882353	0.941176	2.905882	3.025	0.516111	0.49	0.05822
PEKE	4.917647	0.858824	2.552941	2.808219	0.453319	0.428824	0.062983
POM	4.717647	0.929412	3.176471	3.341772	0.576965	0.482941	0.17924
PRES	4.717647	0.964706	3.435294	3.52439	0.616111	0.558824	0.103943
PUG	4.870588	0.776471	2.223529	2.575758	0.397302	0.315882	0.224817
ROTT	4.882353	0.882353	2.670588	2.893333	0.475864	0.44902	0.063943
WOLF	3.847059	0.964706	3.870588	3.97561	0.712773	0.492157	0.345081
Mean	4.730497	0.892451	2.820548	3.018251	0.508899	0.460895	0.108623

*See Table 5 for abbreviations of canid populations.
a = Effective number of individuals sampled from the population (n is smaller than the number of individuals tested due to missing marker data);
P = Proportion of polymorphic loci across all 95 markers for individuals in a population;
A = mean number of alleles per locus;
Ap = mean number of alleles per polymorphic locus;
He = expected heterozygosity;
Ho = observed heterozygosity;
f = estimate of inbreeding coefficient for the population.

TABLE 11

Heterozygosity of 85 Dog Breeds

Population	Heterozygosity
Bedlington Terrier	0.312842
Miniature Bull Terrier	0.321619
Boxer	0.343151
Clumber Spaniel	0.363595
Greater Swiss Mountain Dog	0.364943
Airedale Terrier	0.372793
Soft Coated Wheaten Terrier	0.37376
Collie	0.383453
Doberman Pinscher	0.383763
Irish Terrier	0.390427
Bloodhound	0.391559
German Shepherd Dog	0.397957
Pug Dog	0.398442
Bernese Mountain Dog	0.399599
Flat-coated Retriever	0.402832
Miniature Schnauzer	0.414528
Irish Wolfhound	0.418039
Pharaoh Hound	0.420188
Cavalier King Charles Spaniel	0.427633
Shetland Sheepdog	0.43244
Manchester Terrier Toy	0.432937
French Bulldog	0.439855
Basset Hound	0.441171
American Cocker Spaniel	0.443841
Schipperke	0.445437
Irish Setter	0.446656
Basenji	0.447739
Bulldog	0.449549
Standard Schnauzer	0.450041
Whippet	0.450959
American Hairless Terrier	0.454113
Mastiff	0.455126
Rottweiler	0.45651
Pekingese	0.459983
English Cocker Spaniel	0.46565
Saint Bernard	0.465724
Italian Greyhound	0.468797
Afghan Hound	0.468924
Pointer	0.469444
Shih Tzu	0.472193
Welsh Springer Spaniel	0.473917
Kerry Blue Terrier	0.477836
Dachshund	0.483817
Borzoi	0.487909
Great Dane	0.488697
Alaskan Malamute	0.489877
Newfoundland	0.490617
West Highland White Terrier	0.493936
Belgian Sheepdog	0.495114
Australian Terrier	0.499343
Ibizan Hound	0.503981
Keeshond	0.505126
Bullmastiff	0.509243
Akita	0.510396
Greyhound	0.513409
Chesapeake Bay Retriever	0.514166
Golden Retriever	0.517779
Tibetan Terrier	0.519535
Chow Chow	0.52043
Rhodesian Ridgeback	0.520493
Siberian Husky	0.527344
Bichon Frise	0.528271
Standard Poodle	0.529948
Old English Sheepdog	0.530192
Norwegian Elkhound	0.532854
German Shorthaired Pointer	0.538761
American Water Spaniel	0.540183
Lhasa Apso	0.541245
Samoyed	0.542932
Pomeranian	0.546007
Beagle	0.549119
Border Collie	0.549583
Belgian Tervuren	0.551091
Kuvasz	0.553538
Shiba Inu	0.560543
Labrador Retriever	0.56059
Giant Schnauzer	0.56131
Saluki	0.563037
Portugurese Water Dog	0.568882
Komondor	0.57321
Cairn Terrier	0.575823
Chinese Shar-Pei	0.584412

TABLE 11-continued

Heterozygosity of 85 Dog Breeds

Population	Heterozygosity
Perro de Presa Canario	0.589397
Chihuahua	0.592353
Australian Shepherd	0.609668

TABLE 12

Expected Heterozygosity of 60 Breeds Based on Allele Frequencies at 75 SNP Loci

Breed	Heterozygosity ($\times 10^{-4}$)
Scottish Deerhound	2.0683
Field Spaniel	2.3165
Flat-coated Retriever	2.6474
Bernese Mountain Dog	2.8129
Standard Schnauzer	2.8129
Boxer	3.0611
Collie	3.0611
Bearded Collie	3.1438
Miniature Bull Terrier	3.2266
Perro de Presa Canario	3.392
Bull Terrier	3.8057
Mastiff	3.8057
Petite Basset Griffon Vendeen	3.8884
Bedlington Terrier	3.9712
Saluki	4.1366
Standard Poodle	4.1366
Cavalier King Charles Spaniel	4.2194
Sussex Spaniel	4.2194
American Water Spaniel	4.5503
Ibizan Hound	4.7158
Beagle	4.7985
Boston Terrier	4.7985
German Pinscher	4.8812
Basset Hound	4.964
Bichon Frise	4.964
Rottweiler	4.964
Bullmastiff	5.1294
English Springer Spaniel	5.1294
Greater Swiss Mountain Dog	5.3776
Pug Dog	5.3776
Boykin Spaniel	5.5431
Italian Greyhound	5.5431
Newfoundland	5.5431
American Hairless Terrier	5.7086
Borzoi	5.7913
German Shepherd Dog	5.7913
Saint Bernard	5.7913
Dachshund	5.874
Akita	5.9568
Cocker Spaniel	6.0395
French Bulldog	6.0395
Greyhound	6.0395
Irish Water Spaniel	6.0395
Shetland Sheepdog	6.205
Papillon	6.2877
Foxhound (English)	6.3704
Tibetan Terrier	6.4532
Welsh Springer Spaniel	6.4532
German Shorthaired Pointer	6.6186
Welsh Terrier	6.6186
Dalmatian	6.7014
Irish Setter	6.7014
Alaskan Malamute	6.8668
Golden Retriever	7.0323
Portugese Water Dog	7.115
Weimaraner	7.6942
Labrador Retriever	8.4388
Spinoni Italiano	8.9352
Chesapeake Bay Retriever	9.1006
English Shepherd	9.2661

TABLE 13

Assignments of 346 Canids to 72 Breeds Using Doh

Breed*	Correct	Incorrect
ACKR	3	0
AFGH	3	0
AHRT	5	0
AIRT	4	0
AKIT	5	0
AMAL	5	0
AMWS	5	0
AUSS	5	0
AUST	5	0
BASS	4	0
BEAG	4	1[a]
BEDT	4	0
BELS	3	2[b]
BLDH	5	0
BMD	5	0
BORD	5	0
BORZ	5	0
BOX	5	0
BSJI	5	0
BULD	5	0
BULM	5	0
CAIR	5	0
CHBR	5	0
CHIH	4	1[c]
CKCS	5	0
CLSP	5	0
COLL	5	0
DACH	5	0
DANE	5	0
DNDT	3	0
DOBP	5	0
ECKR	5	0
FCR	5	0
GOLD	5	0
GREY	5	0
GSD	5	0
GSHP	3	2[d]
GSMD	5	0
HUSK	5	0
IBIZ	5	0
IRSE	5	0
IRTR	4	0
IWOF	5	0
KEES	5	0
KOMO	5	0
KUVZ	5	0
LAB	5	0
MAST	5	0
MBLT	5	0
MNTY	4	0
NELK	5	0
NEWF	5	0
OES	3	0
PEKE	5	0
PNTR	5	0
POM	5	0
PRES	5	0
PTWD	5	0
PUG	5	0
RHOD	5	0
ROTT	5	0

TABLE 13-continued

Assignments of 346 Canids to 72 Breeds Using Doh		
Breed*	Correct	Incorrect
SCHP	4	0
SCWT	4	0
SFXT	2	0
SHAR	5	0
SPOO	5	0
SSHP	5	0
STBD	5	0
TERV	1	3[e]
WHIP	5	0
WHWT	5	0
WSSP	5	0

*See Table 5 for abbreviations of canid populations.

[a] 1 dog was misassigned to Presa Canario.

[b] 2 dogs were misassigned to Belgian Tervuren.

[c] 1 dog was misassigned to Cairn Terrier.

[d] 1 dog was misassigned to Kuvasz and 1 dog was misassigned to Standard Poodle.

[e] 3 dogs were misassigned to Belgian Sheepdog.

TABLE 14

Canid	Canid	Missing	Groups									
Population[a]	ID No.	Data	1	2	3	4	5	6	7	8	9	10
AHRT	1124	−2	0.001	0.001	0.001	0.001	0.002	0.001	0.003	0.001	0.002	0.001
AHRT	1120	−1	0.001	0.002	0.002	0.001	0.001	0.001	0.005	0.001	0.001	0.002
AHRT	1121	−4	0.002	0.002	0.003	0.001	0.004	0.001	0.006	0.001	0.001	0.002
AHRT	1123	−2	0.004	0.009	0.038	0.002	0.004	0.005	0.004	0.005	0.003	0.018
AHRT	1122	0	0.008	0.002	0.001	0.008	0.002	0.003	0.002	0.003	0.002	0.002
AKIT	1132	−3	0.001	0.001	0.001	0.975	0.001	0.002	0.001	0.001	0.001	0.001
AKIT	1131	0	0.002	0.003	0.001	0.962	0.002	0.003	0.002	0.006	0.002	0.001
AKIT	1130	−4	0.003	0.001	0.003	0.961	0.001	0.002	0.001	0.001	0.003	0.001
AKIT	1134	−4	0.002	0.001	0.001	0.953	0.002	0.003	0.001	0.014	0.002	0.002
AKIT	1133	−5	0.002	0.001	0.001	0.949	0.001	0.003	0.001	0.001	0.002	0.002
BEAG	995	−1	0.001	0.002	0.003	0.001	0.002	0.001	0.002	0.006	0.001	0.96
BEAG	994	−2	0.001	0.001	0.002	0.001	0.001	0.001	0.014	0.003	0.001	0.939
BEAG	1323	−1	0.005	0.003	0.007	0.003	0.004	0.002	0.004	0.002	0.004	0.909
BEAG	1327	0	0.007	0.002	0.005	0.002	0.002	0.002	0.002	0.001	0.003	0.892
BEAG	1324	0	0.015	0.014	0.002	0.002	0.065	0.016	0.057	0.004	0.015	0.42
BMD	968	−17	0.002	0.002	0.003	0.001	0.001	0.001	0.002	0.001	0.001	0.001
BMD	970	−31	0.002	0.002	0.001	0.003	0.004	0.002	0.003	0.002	0.002	0.002
BMD	941	−11	0.005	0.002	0.002	0.001	0.006	0.002	0.006	0.004	0.002	0.006
BMD	943	−10	0.006	0.007	0.003	0.002	0.003	0.002	0.002	0.003	0.001	0.01
BMD	971	−51	0.017	0.004	0.004	0.002	0.002	0.002	0.002	0.002	0.004	0.002
BOX	1304	−1	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001
BOX	1179	−3	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001
BOX	1178	−1	0.001	0.001	0.002	0.001	0.001	0.001	0.001	0.001	0.001	0.001
BOX	1176	−1	0.002	0.001	0.002	0.001	0.004	0.001	0.002	0.001	0.002	0.002
BOX	1177	0	0.002	0.007	0.008	0.001	0.002	0.003	0.01	0.002	0.004	0.004
BULD	1195	−9	0.002	0.001	0.001	0.001	0.001	0.001	0.002	0.001	0.002	0.001
BULD	1193	−1	0.004	0.003	0.002	0.001	0.001	0.002	0.001	0.001	0.004	0.002
BULD	1197	−3	0.002	0.003	0.002	0.002	0.002	0.002	0.01	0.002	0.001	0.002
BULD	1194	−2	0.004	0.007	0.004	0.002	0.001	0.003	0.006	0.002	0.004	0.003
BULD	1198	0	0.003	0.003	0.001	0.001	0.001	0.001	0.004	0.001	0.004	0.002
PRES	1082	−3	0.008	0.01	0.003	0.002	0.002	0.033	0.002	0.001	0.015	0.025
BULM	1107	−1	0.005	0.004	0.001	0.003	0.003	0.002	0.002	0.006	0.002	0.002
BULM	1109	0	0.002	0.004	0.003	0.004	0.006	0.002	0.003	0.002	0.01	0.002
BULM	1108	0	0.006	0.011	0.006	0.006	0.002	0.006	0.004	0.003	0.013	0.002
BULM	1105	0	0.028	0.006	0.016	0.001	0.004	0.002	0.001	0.001	0.008	0.004
BULM	1106	−3	0.008	0.002	0.04	0.004	0.003	0.005	0.002	0.003	0.031	0.024
MAST	991	−14	0.002	0.001	0.001	0.004	0.002	0.001	0.001	0.001	0.002	0.003
MAST	1066	−2	0.003	0.002	0.002	0.002	0.001	0.002	0.004	0.003	0.003	0.003
MAST	1016	−1	0.003	0.003	0.003	0.001	0.005	0.002	0.002	0.002	0.002	0.001
MAST	1015	0	0.002	0.005	0.008	0.001	0.001	0.002	0.003	0.001	0.002	0.004
MAST	1017	−22	0.002	0.002	0.004	0.001	0.002	0.002	0.001	0.001	0.059	0.001
CHIH	1203	−3	0.002	0.002	0.002	0.002	0.005	0.002	0.003	0.002	0.003	0.002
CHIH	1202	−10	0.006	0.007	0.004	0.001	0.005	0.002	0.005	0.003	0.006	0.012
CHIH	1204	0	0.023	0.037	0.003	0.001	0.004	0.003	0.004	0.004	0.004	0.008
CHIH	1205	−3	0.002	0.028	0.008	0.002	0.004	0.09	0.014	0.065	0.116	0.104
CHIH	1206	−1	0.059	0.125	0.015	0.004	0.012	0.029	0.003	0.025	0.006	0.024
DACH	1052	−2	0.002	0.002	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001
DACH	1055	−1	0.003	0.001	0.002	0.002	0.001	0.001	0.002	0.001	0.004	0.002
DACH	1054	0	0.002	0.002	0.002	0.002	0.001	0.002	0.002	0.001	0.005	0.002
DACH	1051	−5	0.001	0.002	0.003	0.001	0.006	0.002	0.003	0.004	0.003	0.002
DACH	1053	−1	0.004	0.01	0.01	0.001	0.016	0.004	0.003	0.004	0.004	0.012
GOLD	603	0	0.003	0.001	0.967	0.001	0.001	0.001	0.001	0.001	0.001	0.002
GOLD	591	−4	0.009	0.004	0.925	0.002	0.007	0.003	0.004	0.002	0.005	0.005
GOLD	593	0	0.022	0.005	0.885	0.001	0.005	0.003	0.018	0.001	0.006	0.004
GOLD	604	0	0.004	0.003	0.875	0.001	0.009	0.002	0.005	0.001	0.002	0.002

TABLE 14-continued

GOLD	592	−4	0.006	0.006	0.733	0.006	0.009	0.016	0.003	0.002	0.04	0.098
IBIZ	1148	−20	0.001	0.004	0.004	0.001	0.002	0.003	0.002	0.002	0.025	0.002
IBIZ	1172	0	0.021	0.002	0.002	0.002	0.003	0.002	0.002	0.002	0.004	0.002
IBIZ	1162	0	0.003	0.005	0.013	0.002	0.003	0.003	0.002	0.003	0.002	0.002
IBIZ	1280	−1	0.008	0.005	0.004	0.001	0.006	0.002	0.006	0.003	0.004	0.004
IBIZ	1147	−8	0.002	0.001	0.001	0.001	0.003	0.001	0.003	0.003	0.003	0.086
NEWF	275	−3	0.963	0.001	0.002	0.001	0.002	0.001	0.005	0.001	0.002	0.002
NEWF	274	−1	0.953	0.002	0.006	0.001	0.001	0.001	0.002	0.001	0.003	0.003
NEWF	277	0	0.855	0.003	0.002	0.001	0.001	0.002	0.008	0.003	0.002	0.003
NEWF	271	−3	0.848	0.005	0.023	0.002	0.005	0.003	0.027	0.001	0.007	0.002
NEWF	278	−1	0.744	0.007	0.009	0.003	0.002	0.016	0.005	0.004	0.113	0.008
PEKE	1143	0	0.001	0.001	0.001	0.001	0.002	0.001	0.001	0.985	0.001	0.001
PEKE	1145	−1	0.001	0.004	0.002	0.001	0.003	0.002	0.001	0.964	0.001	0.002
PEKE	1211	0	0.001	0.001	0.001	0.004	0.001	0.002	0.003	0.955	0.001	0.002
PEKE	1213	−4	0.001	0.003	0.001	0.001	0.026	0.002	0.003	0.946	0.001	0.001
PEKE	1212	0	0.003	0.005	0.017	0.001	0.001	0.002	0.001	0.932	0.002	0.003
POM	1238	0	0.001	0.964	0.003	0.001	0.004	0.001	0.002	0.003	0.001	0.002
POM	1190	0	0.004	0.794	0.087	0.002	0.003	0.003	0.004	0.005	0.004	0.004
POM	1191	−2	0.051	0.785	0.003	0.002	0.001	0.002	0.005	0.001	0.003	0.003
POM	1210	−7	0.036	0.77	0.013	0.002	0.054	0.004	0.009	0.002	0.012	0.012
POM	1239	−14	0.002	0.598	0.005	0.007	0.006	0.069	0.003	0.014	0.009	0.009
PRES	1093	−14	0.02	0.004	0.002	0.004	0.002	0.005	0.002	0.001	0.865	0.002
PRES	1115	−1	0.008	0.002	0.022	0.001	0.001	0.005	0.003	0.001	0.838	0.002
PRES	1127	−7	0.004	0.008	0.007	0.004	0.002	0.025	0.008	0.002	0.68	0.005
PRES	1096	0	0.007	0.003	0.002	0.001	0.002	0.004	0.003	0.002	0.653	0.004
PUG	1184	−1	0.001	0.001	0.001	0.001	0.988	0.001	0.001	0.001	0.001	0.001
PUG	1077	−4	0.001	0.002	0.002	0.001	0.973	0.001	0.001	0.003	0.001	0.001
PUG	1104	−1	0.001	0.002	0.004	0.001	0.962	0.001	0.001	0.007	0.001	0.002
PUG	1183	−1	0.003	0.001	0.003	0.004	0.96	0.001	0.002	0.002	0.001	0.002
PUG	1192	−3	0.002	0.002	0.001	0.001	0.96	0.001	0.002	0.001	0.003	0.002
ROTT	1034	0	0.002	0.002	0.003	0.001	0.001	0.001	0.952	0.002	0.002	0.003
ROTT	1033	−1	0.004	0.002	0.002	0.001	0.001	0.002	0.951	0.001	0.003	0.002
ROTT	1028	−3	0.002	0.002	0.003	0.001	0.002	0.001	0.95	0.001	0.002	0.016
ROTT	1029	−1	0.015	0.002	0.006	0.002	0.001	0.001	0.917	0.001	0.001	0.005
ROTT	1236	0	0.004	0.022	0.002	0.001	0.002	0.003	0.901	0.002	0.007	0.007
ROTT	1014	−2	0.048	0.002	0.004	0.002	0.004	0.002	0.898	0.002	0.002	0.006
WOLF	282135	−1	0.001	0.001	0.001	0.001	0.001	0.002	0.002	0.002	0.001	0.001
WOLF	930121	−3	0.001	0.002	0.001	0.008	0.001	0.002	0.001	0.003	0.001	0.001
WOLF	492	−1	0.001	0.002	0.001	0.002	0.002	0.559	0.001	0.002	0.005	0.001
WOLF	Iran	−7	0.001	0.001	0.002	0.002	0.002	0.741	0.001	0.003	0.002	0.002

Canid	Canid	Missing	Groups									
Population[a]	ID No.	Data	11	12	13	14	15	16	17	18	19	20
AHRT	1124	−2	0.002	0.001	0.001	0.002	0.001	0.001	0.001	0.001	0.001	0.972
AHRT	1120	−1	0.002	0.001	0.001	0.004	0.002	0.001	0.001	0.002	0.002	0.966
AHRT	1121	−4	0.002	0.001	0.003	0.001	0.002	0.001	0.001	0.001	0.002	0.963
AHRT	1123	−2	0.007	0.003	0.019	0.004	0.012	0.015	0.003	0.002	0.004	0.84
AHRT	1122	0	0.048	0.002	0.009	0.016	0.003	0.002	0.002	0.002	0.059	0.825
AKIT	1132	−3	0.002	0.001	0.002	0.001	0.002	0.001	0.002	0.001	0.001	0.002
AKIT	1131	0	0.002	0.002	0.001	0.001	0.001	0.001	0.002	0.001	0.002	0.003
AKIT	1130	−4	0.003	0.002	0.002	0.002	0.003	0.001	0.005	0.002	0.002	0.001
AKIT	1134	−4	0.002	0.001	0.003	0.001	0.001	0.001	0.003	0.001	0.001	0.004
AKIT	1133	−5	0.001	0.025	0.001	0.001	0.002	0.001	0.001	0.001	0.002	0.001
BEAG	995	−1	0.002	0.001	0.002	0.002	0.001	0.001	0.001	0.001	0.002	0.005
BEAG	994	−2	0.002	0.001	0.001	0.022	0.001	0.001	0.001	0.002	0.001	0.002
BEAG	1323	−1	0.007	0.001	0.005	0.003	0.006	0.008	0.002	0.006	0.007	0.013
BEAG	1327	0	0.004	0.002	0.002	0.005	0.002	0.048	0.002	0.008	0.006	0.002
BEAG	1324	0	0.01	0.005	0.003	0.002	0.002	0.001	0.086	0.005	0.002	0.274
BMD	968	−17	0.001	0.001	0.001	0.002	0.002	0.001	0.001	0.002	0.972	0.001
BMD	970	−31	0.003	0.005	0.002	0.003	0.002	0.001	0.002	0.002	0.956	0.002
BMD	941	−11	0.003	0.002	0.002	0.001	0.002	0.009	0.002	0.004	0.937	0.001
BMD	943	−10	0.004	0.001	0.005	0.007	0.002	0.002	0.001	0.002	0.934	0.003
BMD	971	−51	0.003	0.003	0.003	0.003	0.002	0.003	0.002	0.003	0.933	0.006
BOX	1304	−1	0.001	0.001	0.001	0.001	0.001	0.983	0.001	0.001	0.001	0.001
BOX	1179	−3	0.001	0.001	0.001	0.001	0.001	0.982	0.001	0.001	0.001	0.001
BOX	1178	−1	0.001	0.001	0.001	0.001	0.002	0.978	0.001	0.002	0.001	0.001
BOX	1176	−1	0.001	0.001	0.002	0.001	0.001	0.972	0.001	0.001	0.001	0.002
BOX	1177	0	0.012	0.001	0.003	0.037	0.004	0.889	0.001	0.003	0.003	0.004
BULD	1195	−9	0.001	0.001	0.002	0.001	0.004	0.003	0.001	0.974	0.001	0.001
BULD	1193	−1	0.002	0.002	0.002	0.002	0.006	0.002	0.001	0.96	0.001	0.001
BULD	1197	−3	0.002	0.004	0.005	0.001	0.002	0.003	0.004	0.948	0.002	0.002
BULD	1194	−2	0.002	0.001	0.002	0.01	0.006	0.004	0.002	0.935	0.001	0.002
BULD	1198	0	0.005	0.001	0.003	0.002	0.005	0.004	0.001	0.912	0.043	0.002
PRES	1082	−3	0.151	0.206	0.002	0.023	0.293	0.008	0.003	0.199	0.004	0.009
BULM	1107	−1	0.005	0.001	0.005	0.001	0.95	0.002	0.001	0.002	0.002	0.001
BULM	1109	0	0.002	0.001	0.004	0.001	0.932	0.013	0.002	0.005	0.001	0.002
BULM	1108	0	0.003	0.001	0.005	0.002	0.894	0.002	0.01	0.009	0.007	0.009

TABLE 14-continued

BULM	1105	0	0.011	0.002	0.002	0.008	0.87	0.012	0.002	0.012	0.004	0.004
BULM	1106	−3	0.002	0.003	0.004	0.002	0.823	0.004	0.017	0.017	0.003	0.004
MAST	991	−14	0.002	0.001	0.002	0.006	0.963	0.001	0.001	0.001	0.002	0.002
MAST	1066	−2	0.003	0.001	0.002	0.003	0.948	0.003	0.001	0.007	0.003	0.005
MAST	1016	−1	0.004	0.002	0.003	0.003	0.93	0.001	0.002	0.025	0.006	0.001
MAST	1015	0	0.002	0.001	0.002	0.019	0.929	0.002	0.001	0.003	0.006	0.004
MAST	1017	−22	0.002	0.001	0.025	0.001	0.885	0.001	0.001	0.002	0.003	0.003
CHIH	1203	−3	0.932	0.003	0.009	0.003	0.002	0.003	0.003	0.003	0.014	0.003
CHIH	1202	−10	0.916	0.001	0.003	0.005	0.005	0.003	0.002	0.004	0.001	0.007
CHIH	1204	0	0.868	0.002	0.004	0.002	0.003	0.002	0.002	0.003	0.018	0.005
CHIH	1205	−3	0.455	0.008	0.032	0.004	0.012	0.003	0.023	0.022	0.001	0.006
CHIH	1206	−1	0.436	0.003	0.016	0.008	0.033	0.152	0.006	0.006	0.006	0.031
DACH	1052	−2	0.001	0.001	0.001	0.976	0.003	0.001	0.001	0.002	0.001	0.001
DACH	1055	−1	0.003	0.001	0.002	0.958	0.002	0.005	0.002	0.002	0.004	0.002
DACH	1054	0	0.002	0.002	0.002	0.951	0.002	0.014	0.001	0.003	0.002	0.002
DACH	1051	−5	0.003	0.001	0.004	0.949	0.004	0.002	0.002	0.002	0.002	0.005
DACH	1053	−1	0.011	0.002	0.005	0.892	0.002	0.004	0.002	0.01	0.002	0.003
GOLD	603	0	0.001	0.001	0.002	0.001	0.002	0.002	0.001	0.002	0.006	0.001
GOLD	591	−4	0.002	0.001	0.003	0.004	0.011	0.004	0.004	0.004	0.001	0.003
GOLD	593	0	0.002	0.001	0.003	0.027	0.002	0.004	0.001	0.003	0.003	0.005
GOLD	604	0	0.002	0.001	0.002	0.003	0.003	0.072	0.001	0.004	0.002	0.004
GOLD	592	−4	0.002	0.003	0.003	0.021	0.012	0.004	0.006	0.002	0.003	0.022
IBIZ	1148	−20	0.002	0.002	0.929	0.001	0.004	0.001	0.009	0.002	0.001	0.003
IBIZ	1172	0	0.004	0.001	0.917	0.016	0.003	0.002	0.001	0.003	0.009	0.004
IBIZ	1162	0	0.03	0.001	0.913	0.001	0.004	0.003	0.001	0.003	0.002	0.003
IBIZ	1280	−1	0.002	0.001	0.888	0.002	0.006	0.036	0.004	0.005	0.007	0.003
IBIZ	1147	−8	0.007	0.001	0.871	0.001	0.003	0.002	0.001	0.005	0.002	0.002
NEWF	275	−3	0.002	0.001	0.002	0.002	0.002	0.004	0.001	0.002	0.004	0.001
NEWF	274	−1	0.002	0.001	0.007	0.001	0.003	0.003	0.001	0.003	0.001	0.003
NEWF	277	0	0.002	0.002	0.001	0.002	0.076	0.028	0.001	0.002	0.002	0.003
NEWF	271	−3	0.034	0.002	0.004	0.003	0.002	0.003	0.001	0.016	0.008	0.003
NEWF	278	−1	0.011	0.002	0.011	0.018	0.029	0.003	0.004	0.004	0.006	0.001
PEKE	1143	0	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001
PEKE	1145	−1	0.003	0.002	0.002	0.002	0.001	0.001	0.002	0.001	0.001	0.003
PEKE	1211	0	0.007	0.004	0.002	0.002	0.002	0.004	0.001	0.002	0.002	0.003
PEKE	1213	−4	0.001	0.001	0.002	0.001	0.001	0.001	0.001	0.001	0.002	0.003
PEKE	1212	0	0.003	0.001	0.003	0.002	0.005	0.011	0.002	0.002	0.002	0.001
POM	1238	0	0.002	0.001	0.001	0.002	0.002	0.001	0.002	0.001	0.002	0.001
POM	1190	0	0.018	0.003	0.003	0.001	0.003	0.004	0.003	0.005	0.034	0.015
POM	1191	−2	0.006	0.001	0.002	0.004	0.097	0.006	0.002	0.022	0.002	0.001
POM	1210	−7	0.003	0.01	0.006	0.007	0.002	0.012	0.004	0.035	0.005	0.002
POM	1239	−14	0.004	0.002	0.232	0.007	0.004	0.003	0.004	0.007	0.005	0.01
PRES	1093	−14	0.004	0.008	0.01	0.002	0.028	0.022	0.003	0.01	0.002	0.004
PRES	1115	−1	0.003	0.002	0.002	0.003	0.01	0.066	0.009	0.01	0.001	0.01
PRES	1127	−7	0.008	0.002	0.067	0.016	0.008	0.012	0.006	0.123	0.003	0.01
PRES	1096	0	0.003	0.002	0.004	0.105	0.019	0.019	0.006	0.145	0.008	0.007
PUG	1184	−1	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001
PUG	1077	−4	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.004
PUG	1104	−1	0.001	0.001	0.002	0.001	0.003	0.002	0.001	0.001	0.002	0.002
PUG	1183	−1	0.001	0.001	0.008	0.001	0.002	0.001	0.001	0.001	0.002	0.002
PUG	1192	−3	0.002	0.001	0.003	0.001	0.001	0.006	0.002	0.003	0.003	0.002
ROTT	1034	0	0.003	0.001	0.003	0.004	0.001	0.006	0.001	0.003	0.005	0.002
ROTT	1033	−1	0.002	0.001	0.002	0.003	0.003	0.003	0.002	0.007	0.001	0.008
ROTT	1028	−3	0.001	0.001	0.001	0.007	0.001	0.005	0.001	0.001	0.001	0.001
ROTT	1029	−1	0.002	0.001	0.001	0.004	0.002	0.001	0.001	0.001	0.034	0.002
ROTT	1236	0	0.003	0.003	0.004	0.01	0.002	0.006	0.003	0.016	0.001	0.001
ROTT	1014	−2	0.004	0.002	0.004	0.001	0.004	0.001	0.002	0.003	0.006	0.003
WOLF	282135	−1	0.001	0.979	0.001	0.001	0.001	0.001	0.002	0.001	0.001	0.001
WOLF	930121	−3	0.001	0.032	0.001	0.001	0.001	0.001	0.938	0.001	0.001	0.001
WOLF	492	−1	0.001	0.044	0.001	0.001	0.001	0.001	0.371	0.001	0.001	0.001
WOLF	Iran	−7	0.002	0.022	0.002	0.004	0.003	0.001	0.203	0.001	0.001	0.002

[a] See Table 5 for abbreviations of canid populations.
KBB: pbe

TABLE 15A

Canid	Canid ID	Missing	Groups					
Population[a]	No.	Data	1	2	3	4	5	6
WOLF	4928	−1	0	0.999	0	0.001	0	0
WOLF	282135	−1	0	0.998	0	0.002	0	0
WOLF	930121	−3	0	0.997	0	0.003	0	0
WOLF	Iran1	−7	0	0.999	0	0.001	0	0
AKIT	1130	−4	0	0.005	0	0.995	0	0
AKIT	1131	0	0	0.013	0	0.987	0	0

TABLE 15A-continued

Canid Population^a	Canid ID No.	Missing Data	Groups 1	2	3	4	5	6
AKIT	1132	−3	0	0.004	0	0.996	0	0
AKIT	1133	−5	0	0.005	0	0.995	0	0
AKIT	1134	−4	0	0.007	0	0.993	0	0
PEKE	1143	0	0	0	0.999	0.001	0	0
PEKE	1145	−1	0	0	0.992048	0.007952	0	0
PEKE	1211	0	0	0	0.947818	0.052182	0	0
PEKE	1212	0	0	0	0.961501	0.038499	0	0
PEKE	1213	−4	0	0	0.997994	0.002006	0	0
PUG	1077	−4	0	0	0	0.002	0.998	0
PUG	1104	−1	0	0	0	0.006	0.994	0
PUG	1183	−1	0	0	0	0.002	0.998	0
PUG	1184	−1	0	0	0	0.001	0.999	0
PUG	1192	−3	0	0	0	0.001	0.999	0
GOLD	591	−4	0.021339	0	0	0.030068	0	0.948594
GOLD	592	−4	0.004314	0	0	0.137187	0	0.858499
GOLD	593	0	0.005935	0	0	0.01088	0	0.983185
GOLD	603	0	0.008929	0	0	0.007937	0	0.983135
GOLD	604	0	0.037624	0	0	0.009901	0	0.952475
AHRT	1120	−1	0.006289	0	0	0.213836	0	0.779874
AHRT	1121	−4	0.003885	0	0	0.222999	0	0.773116
AHRT	1122	0	0.003079	0	0	0.230177	0	0.766744
AHRT	1123	−2	0.016419	0	0	0.218139	0	0.765442
AHRT	1124	−2	0.004594	0	0	0.234303	0	0.761103
CHIH	1202	−10	0.008326	0	0	0.074931	0	0.916744
CHIH	1203	−3	0.005578	0	0	0.203187	0	0.791235
CHIH	1204	0	0.004184	0	0	0.16318	0	0.832636
CHIH	1205	−3	0.021598	0	0	0.280058	0	0.698344
CHIH	1206	−1	0.097854	0	0	0.141631	0	0.760515
POM	1190	0	0.038938	0	0	0.115044	0	0.846018
POM	1191	−2	0.480901	0	0	0.020568	0	0.498531
POM	1210	−7	0.020236	0	0	0.15683	0	0.822934
POM	1238	0	0.006961	0	0	0.226605	0	0.766435
POM	1239	−14	0.006266	0	0	0.373434	0	0.620301
DACH	1051	−5	0.008145	0	0	0.095023	0	0.896833
DACH	1052	−2	0.013889	0	0	0.007937	0	0.978175
DACH	1053	−1	0.009747	0	0	0.025341	0	0.964912
DACH	1054	0	0.006917	0	0	0.011858	0	0.981225
DACH	1055	−1	0.010848	0	0	0.013807	0	0.975345
BEAG	994	−2	0.004869	0	0	0.02629	0	0.968841
BEAG	995	−1	0.002681	0	0	0.106345	0	0.890974
BEAG	1323	−1	0.009747	0	0	0.025341	0	0.964912
BEAG	1324	0	0.002839	0	0	0.290277	0	0.706884
BEAG	1327	0	0.01256	0	0	0.033816	0	0.953623
IBIZ	1147	−8	0.011867	0	0	0.208861	0	0.779272
IBIZ	1148	−20	0.01225	0	0	0.355255	0	0.632495
IBIZ	1162	0	0.019639	0	0	0.214454	0	0.765907
IBIZ	1172	0	0.00639	0	0	0.201278	0	0.792332
IBIZ	1280	−1	0.023682	0	0	0.236058	0	0.74026
BMD	941	−11	0.009709	0	0	0.029126	0	0.961165
BMD	943	−10	0.006686	0	0	0.04489	0	0.948424
BMD	968	−17	0.005831	0	0	0.028183	0	0.965986
BMD	970	−31	0.011354	0	0	0.18897	0	0.799676
BMD	971	−51	0.020568	0	0	0.020568	0	0.958864
NEWF	271	−3	0.010913	0	0	0.007937	0	0.981151
NEWF	274	−1	0.019881	0	0	0.005964	0	0.974155
NEWF	275	−3	0.010934	0	0	0.005964	0	0.983101
NEWF	277	0	0.05859	0	0	0.006951	0	0.934459
NEWF	278	−1	0.034213	0	0	0.022483	0	0.943304
ROTT	1014	−2	0.0059	0	0	0.016716	0	0.977384
ROTT	1028	−3	0.005946	0	0	0.00892	0	0.985134
ROTT	1029	−1	0.004955	0	0	0.00892	0	0.986125
ROTT	1033	−1	0.009728	0	0	0.027237	0	0.963035
ROTT	1034	0	0.021782	0	0	0.009901	0	0.968317
PRES	1082	−3	0.419635	0	0	0.13119	0	0.449175
PRES	1093	−14	0.430979	0	0	0.197432	0	0.371589
PRES	1096	0	0.705253	0	0	0.027237	0	0.26751
PRES	1115	−1	0.572519	0	0	0.045802	0	0.381679
PRES	1127	−7	0.418004	0	0	0.108734	0	0.473262
BOX	1176	−1	0.98806	0	0	0.004975	0	0.006965
BOX	1177	0	0.964108	0	0	0.002991	0	0.032901
BOX	1178	−1	0.993028	0	0	0.003984	0	0.002988
BOX	1179	−3	0.993028	0	0	0.003984	0	0.002988
BOX	1304	−1	0.989066	0	0	0.005964	0	0.00497
BULD	1193	−1	0.971202	0	0	0.006951	0	0.021847
BULD	1194	−2	0.989044	0	0	0.003984	0	0.006972

TABLE 15A-continued

Canid	Canid ID	Missing	Groups					
Population^{a}	No.	Data	1	2	3	4	5	6
BULD	1195	−9	0.99005	0	0	0.004975	0	0.004975
BULD	1197	−3	0.879648	0	0	0.021526	0	0.098826
BULD	1198	0	0.983051	0	0	0.002991	0	0.013958
MAST	991	−14	0.97931	0	0	0.014778	0	0.005911
MAST	1015	0	0.983085	0	0	0.004975	0	0.01194
MAST	1016	−1	0.981188	0	0	0.009901	0	0.008911
MAST	1017	−22	0.94294	0	0	0.032882	0	0.024178
MAST	1066	−2	0.983168	0	0	0.009901	0	0.006931
BULM	1105	0	0.985075	0	0	0.004975	0	0.00995
BULM	1106	−3	0.971429	0	0	0.014778	0	0.013793
BULM	1107	−1	0.973529	0	0	0.019608	0	0.006863
BULM	1108	0	0.970559	0	0	0.018646	0	0.010795
BULM	1109	0	0.974535	0	0	0.020568	0	0.004897

TABLE 15B

Canid	Canid ID	Missing	Groups					
Population^{a}	No.	Data	1	2	3	4	5	6
WOLF	4928	−1	0	0.999	0	0.001	0	0
WOLF	282135	−1	0	0.998	0	0.002	0	0
WOLF	930121	−3	0	0.997	0	0.003	0	0
WOLF	Iran1	−7	0	0.999	0	0.001	0	0
AKIT	1130	−4	0	0.005	0	0.995	0	0
AKIT	1131	0	0	0.013	0	0.987	0	0
AKIT	1132	−3	0	0.004	0	0.996	0	0
AKIT	1133	−5	0	0.005	0	0.995	0	0
AKIT	1134	−4	0	0.007	0	0.993	0	0
PEKE	1143	0	0	0	0.999	0.001	0	0
PEKE	1145	−1	0	0	0.992048	0.007952	0	0
PEKE	1211	0	0	0	0.947818	0.052182	0	0
PEKE	1212	0	0	0	0.961501	0.038499	0	0
PEKE	1213	−4	0	0	0.997994	0.002006	0	0
PUG	1077	−4	0	0	0	0.002	0.998	0
PUG	1104	−1	0	0	0	0.006	0.994	0
PUG	1183	−1	0	0	0	0.002	0.998	0
PUG	1184	−1	0	0	0	0.001	0.999	0
PUG	1192	−3	0	0	0	0.001	0.999	0
GOLD	591	−4	0.021339	0	0	0.030068	0	0.948594
GOLD	592	−4	0.004314	0	0	0.137187	0	0.858499
GOLD	593	0	0.005935	0	0	0.01088	0	0.983185
GOLD	603	0	0.008929	0	0	0.007937	0	0.983135
GOLD	604	0	0.037624	0	0	0.009901	0	0.952475
AHRT	1120	−1	0.006289	0	0	0.213836	0	0.779874
AHRT	1121	−4	0.003885	0	0	0.222999	0	0.773116
AHRT	1122	0	0.003079	0	0	0.230177	0	0.766744
AHRT	1123	−2	0.016419	0	0	0.218139	0	0.765442
AHRT	1124	−2	0.004594	0	0	0.234303	0	0.761103
CHIH	1202	−10	0.008326	0	0	0.074931	0	0.916744
CHIH	1203	−3	0.005578	0	0	0.203187	0	0.791235
CHIH	1204	0	0.004184	0	0	0.16318	0	0.832636
CHIH	1205	−3	0.021598	0	0	0.280058	0	0.698344
CHIH	1206	−1	0.097854	0	0	0.141631	0	0.760515
POM	1190	0	0.038938	0	0	0.115044	0	0.846018
POM	1191	−2	0.480901	0	0	0.020568	0	0.498531
POM	1210	−7	0.020236	0	0	0.15683	0	0.822934
POM	1238	0	0.006961	0	0	0.226605	0	0.766435
POM	1239	−14	0.006266	0	0	0.373434	0	0.620301
DACH	1051	−5	0.008145	0	0	0.095023	0	0.896833
DACH	1052	−2	0.013889	0	0	0.007937	0	0.978175
DACH	1053	−1	0.009747	0	0	0.025341	0	0.964912
DACH	1054	0	0.006917	0	0	0.011858	0	0.981225
DACH	1055	−1	0.010848	0	0	0.013807	0	0.975345
BEAG	994	−2	0.004869	0	0	0.02629	0	0.968841
BEAG	995	−1	0.002681	0	0	0.106345	0	0.890974
BEAG	1323	−1	0.009747	0	0	0.025341	0	0.964912
BEAG	1324	0	0.002839	0	0	0.290277	0	0.706884
BEAG	1327	0	0.01256	0	0	0.033816	0	0.953623
IBIZ	1147	−8	0.011867	0	0	0.208861	0	0.779272
IBIZ	1148	−20	0.01225	0	0	0.355255	0	0.632495
IBIZ	1162	0	0.019639	0	0	0.214454	0	0.765907

TABLE 15B-continued

Canid Population^a	Canid ID No.	Missing Data	Groups 1	2	3	4	5	6
IBIZ	1172	0	0.00639	0	0	0.201278	0	0.792332
IBIZ	1280	−1	0.023682	0	0	0.236058	0	0.74026
BMD	941	−11	0.009709	0	0	0.029126	0	0.961165
BMD	943	−10	0.006686	0	0	0.04489	0	0.948424
BMD	968	−17	0.005831	0	0	0.028183	0	0.965986
BMD	970	−31	0.011354	0	0	0.18897	0	0.799676
BMD	971	−51	0.020568	0	0	0.020568	0	0.958864
NEWF	271	−3	0.010913	0	0	0.007937	0	0.981151
NEWF	274	−1	0.019881	0	0	0.005964	0	0.974155
NEWF	275	−3	0.010934	0	0	0.005964	0	0.983101
NEWF	277	0	0.05859	0	0	0.006951	0	0.934459
NEWF	278	−1	0.034213	0	0	0.022483	0	0.943304
ROTT	1014	−2	0.0059	0	0	0.016716	0	0.977384
ROTT	1028	−3	0.005946	0	0	0.00892	0	0.985134
ROTT	1029	−1	0.004955	0	0	0.00892	0	0.986125
ROTT	1033	−1	0.009728	0	0	0.027237	0	0.963035
ROTT	1034	0	0.021782	0	0	0.009901	0	0.968317
PRES	1082	−3	0.419635	0	0	0.13119	0	0.449175
PRES	1093	−14	0.430979	0	0	0.197432	0	0.371589
PRES	1096	0	0.705253	0	0	0.027237	0	0.26751
PRES	1115	−1	0.572519	0	0	0.045802	0	0.381679
PRES	1127	−7	0.418004	0	0	0.108734	0	0.473262
BOX	1176	−1	0.002964	0	0	0.004941	0	0.006917
BOX	1177	0	0.046332	0	0	0.002896	0	0.031853
BOX	1178	−1	0.002979	0	0	0.003972	0	0.002979
BOX	1179	−3	0.000993	0	0	0.003972	0	0.002979
BOX	1304	−1	0.001978	0	0	0.005935	0	0.004946
BULD	1193	−1	0.968902	0	0	0.006803	0	0.02138
BULD	1194	−2	0.986152	0	0	0.003956	0	0.006924
BULD	1195	−9	0.988119	0	0	0.00495	0	0.00495
BULD	1197	−3	0.887801	0	0	0.01959	0	0.089938
BULD	1198	0	0.979351	0	0	0.00295	0	0.013766
MAST	991	−14	0.978452	0	0	0.014691	0	0.005877
MAST	1015	0	0.981318	0	0	0.004916	0	0.011799
MAST	1016	−1	0.980373	0	0	0.009814	0	0.008832
MAST	1017	−22	0.943343	0	0	0.032106	0	0.023607
MAST	1066	−2	0.981318	0	0	0.009833	0	0.006883
BULM	1105	0	0.981281	0	0	0.004926	0	0.009852
BULM	1106	−3	0.969874	0	0	0.014577	0	0.013605
BULM	1107	−1	0.971762	0	0	0.019474	0	0.006816
BULM	1108	0	0.969903	0	0	0.018447	0	0.01068
BULM	1109	0	0.971735	0	0	0.020468	0	0.004873

TABLE 15C

Canid Population^a	Canid ID No.	Missing Data	Groups 1	2	3	4	5	6
WOLF	4928	−1	0	0.999	0	0.001	0	0
WOLF	282135	−1	0	0.998	0	0.002	0	0
WOLF	930121	−3	0	0.997	0	0.003	0	0
WOLF	Iran1	−7	0	0.999	0	0.001	0	0
AKIT	1130	−4	0	0.005	0	0.995	0	0
AKIT	1131	0	0	0.013	0	0.987	0	0
AKIT	1132	−3	0	0.004	0	0.996	0	0
AKIT	1133	−5	0	0.005	0	0.995	0	0
AKIT	1134	−4	0	0.007	0	0.993	0	0
PEKE	1143	0	0	0	0.999	0.001	0	0
PEKE	1145	−1	0	0	0.992048	0.007952	0	0
PEKE	1211	0	0	0	0.947818	0.052182	0	0
PEKE	1212	0	0	0	0.961501	0.038499	0	0
PEKE	1213	−4	0	0	0.997994	0.002006	0	0
PUG	1077	−4	0	0	0	0.002	0.998	0
PUG	1104	−1	0	0	0	0.006	0.994	0
PUG	1183	−1	0	0	0	0.002	0.998	0
PUG	1184	−1	0	0	0	0.001	0.999	0
PUG	1192	−3	0	0	0	0.001	0.999	0
GOLD	591	−4	0.021339	0	0	0.030068	0	0.948594
GOLD	592	−4	0.004314	0	0	0.137187	0	0.858499
GOLD	593	0	0.005935	0	0	0.01088	0	0.983185
GOLD	603	0	0.008929	0	0	0.007937	0	0.983135

TABLE 15C-continued

Canid	Canid ID	Missing	Groups					
Population[a]	No.	Data	1	2	3	4	5	6
GOLD	604	0	0.037624	0	0	0.009901	0	0.952475
AHRT	1120	−1	0.006289	0	0	0.213836	0	0.779874
AHRT	1121	−4	0.003885	0	0	0.222999	0	0.773116
AHRT	1122	0	0.003079	0	0	0.230177	0	0.766744
AHRT	1123	−2	0.016419	0	0	0.218139	0	0.765442
AHRT	1124	−2	0.004594	0	0	0.234303	0	0.761103
CHIH	1202	−10	0.008326	0	0	0.074931	0	0.916744
CHIH	1203	−3	0.005578	0	0	0.203187	0	0.791235
CHIH	1204	0	0.004184	0	0	0.16318	0	0.832636
CHIH	1205	−3	0.021598	0	0	0.280058	0	0.698344
CHIH	1206	−1	0.097854	0	0	0.141631	0	0.760515
POM	1190	0	0.038938	0	0	0.115044	0	0.846018
POM	1191	−2	0.480901	0	0	0.020568	0	0.498531
POM	1210	−7	0.020236	0	0	0.15683	0	0.822934
POM	1238	0	0.006961	0	0	0.226605	0	0.766435
POM	1239	−14	0.006266	0	0	0.373434	0	0.620301
DACH	1051	−5	0.008145	0	0	0.095023	0	0.896833
DACH	1052	−2	0.013889	0	0	0.007937	0	0.978175
DACH	1053	−1	0.009747	0	0	0.025341	0	0.964912
DACH	1054	0	0.006917	0	0	0.011858	0	0.981225
DACH	1055	−1	0.010848	0	0	0.013807	0	0.975345
BEAG	994	−2	0.004869	0	0	0.02629	0	0.968841
BEAG	995	−1	0.002681	0	0	0.106345	0	0.890974
BEAG	1323	−1	0.009747	0	0	0.025341	0	0.964912
BEAG	1324	0	0.002839	0	0	0.290277	0	0.706884
BEAG	1327	0	0.01256	0	0	0.033816	0	0.953623
IBIZ	1147	−8	0.011867	0	0	0.208861	0	0.779272
IBIZ	1148	−20	0.01225	0	0	0.355255	0	0.632495
IBIZ	1162	0	0.019639	0	0	0.214454	0	0.765907
IBIZ	1172	0	0.00639	0	0	0.201278	0	0.792332
IBIZ	1280	−1	0.023682	0	0	0.236058	0	0.74026
BMD	941	−11	0.009709	0	0	0.029126	0	0.961165
BMD	943	−10	0.006686	0	0	0.04489	0	0.948424
BMD	968	−17	0.005831	0	0	0.028183	0	0.965986
BMD	970	−31	0.011354	0	0	0.18897	0	0.799676
BMD	971	−51	0.020568	0	0	0.020568	0	0.958864
NEWF	271	−3	0.010913	0	0	0.007937	0	0.981151
NEWF	274	−1	0.019881	0	0	0.005964	0	0.974155
NEWF	275	−3	0.010934	0	0	0.005964	0	0.983101
NEWF	277	0	0.05859	0	0	0.006951	0	0.934459
NEWF	278	−1	0.034213	0	0	0.022483	0	0.943304
ROTT	1014	−2	0.0059	0	0	0.016716	0	0.977384
ROTT	1028	−3	0.005946	0	0	0.00892	0	0.985134
ROTT	1029	−1	0.004955	0	0	0.00892	0	0.986125
ROTT	1033	−1	0.009728	0	0	0.027237	0	0.963035
ROTT	1034	0	0.021782	0	0	0.009901	0	0.968317
PRES	1082	−3	0.419635	0	0	0.13119	0	0.449175
PRES	1093	−14	0.430979	0	0	0.197432	0	0.371589
PRES	1096	0	0.705253	0	0	0.027237	0	0.26751
PRES	1115	−1	0.572519	0	0	0.045802	0	0.381679
PRES	1127	−7	0.418004	0	0	0.108734	0	0.473262
BOX	1176	−1	0.002964	0	0	0.004941	0	0.006917
BOX	1177	0	0.046332	0	0	0.002896	0	0.031853
BOX	1178	−1	0.002979	0	0	0.003972	0	0.002979
BOX	1179	−3	0.000993	0	0	0.003972	0	0.002979
BOX	1304	−1	0.001978	0	0	0.005935	0	0.004946
BULD	1193	−1	0.001938	0	0	0.006783	0	0.021318
BULD	1194	−2	0.004931	0	0	0.003945	0	0.006903
BULD	1195	−9	0.000988	0	0	0.004941	0	0.004941
BULD	1197	−3	0.003552	0	0	0.019538	0	0.089698
BULD	1198	0	0.003918	0	0	0.002938	0	0.013712
MAST	991	−14	0.976517	0	0	0.014677	0	0.005871
MAST	1015	0	0.979392	0	0	0.004907	0	0.011776
MAST	1016	−1	0.972549	0	0	0.009804	0	0.008824
MAST	1017	−22	0.941509	0	0	0.032075	0	0.023585
MAST	1066	−2	0.975466	0	0	0.009814	0	0.006869
BULM	1105	0	0.976447	0	0	0.004907	0	0.009814
BULM	1106	−3	0.964113	0	0	0.014549	0	0.013579
BULM	1107	−1	0.969874	0	0	0.019436	0	0.006803
BULM	1108	0	0.967022	0	0	0.018429	0	0.010669
BULM	1109	0	0.968902	0	0	0.020408	0	0.004859

TABLE 15D

Canid	Canid ID	Missing	Groups								
Population^a	No.	Data	1	2	3	4	5	6	7	8	9
WOLF	4928	−1	0	0.999	0	0.001	0	0	0	0	0
WOLF	282135	−1	0	0.998	0	0.002	0	0	0	0	0
WOLF	930121	−3	0	0.997	0	0.003	0	0	0	0	0
WOLF	Iran1	−7	0	0.999	0	0.001	0	0	0	0	0
AKIT	1130	−4	0	0.005	0	0.995	0	0	0	0	0
AKIT	1131	0	0	0.013	0	0.987	0	0	0	0	0
AKIT	1132	−3	0	0.004	0	0.996	0	0	0	0	0
AKIT	1133	−5	0	0.005	0	0.995	0	0	0	0	0
AKIT	1134	−4	0	0.007	0	0.993	0	0	0	0	0
PEKE	1143	0	0	0	0.999	0.001	0	0	0	0	0
PEKE	1145	−1	0	0	0.992048	0.007952	0	0	0	0	0
PEKE	1211	0	0	0	0.947818	0.052182	0	0	0	0	0
PEKE	1212	0	0	0	0.961501	0.038499	0	0	0	0	0
PEKE	1213	−4	0	0	0.997994	0.002006	0	0	0	0	0
PUG	1077	−4	0	0	0	0.002	0.998	0	0	0	0
PUG	1104	−1	0	0	0	0.006	0.994	0	0	0	0
PUG	1183	−1	0	0	0	0.002	0.998	0	0	0	0
PUG	1184	−1	0	0	0	0.001	0.999	0	0	0	0
PUG	1192	−3	0	0	0	0.001	0.999	0	0	0	0
GOLD	591	−4	0.021339	0	0	0.030068	0	0.948594	0	0	0
GOLD	592	−4	0.004314	0	0	0.137187	0	0.858499	0	0	0
GOLD	593	0	0.005935	0	0	0.01088	0	0.983185	0	0	0
GOLD	603	0	0.008929	0	0	0.007937	0	0.983135	0	0	0
GOLD	604	0	0.037624	0	0	0.009901	0	0.952475	0	0	0
AHRT	1120	−1	0.006289	0	0	0.213836	0	0.779874	0	0	0
AHRT	1121	−4	0.003885	0	0	0.222999	0	0.773116	0	0	0
AHRT	1122	0	0.003079	0	0	0.230177	0	0.766744	0	0	0
AHRT	1123	−2	0.016419	0	0	0.218139	0	0.765442	0	0	0
AHRT	1124	−2	0.004594	0	0	0.234303	0	0.761103	0	0	0
CHIH	1202	−10	0.008326	0	0	0.074931	0	0.916744	0	0	0
CHIH	1203	−3	0.005578	0	0	0.203187	0	0.791235	0	0	0
CHIH	1204	0	0.004184	0	0	0.16318	0	0.832636	0	0	0
CHIH	1205	−3	0.021598	0	0	0.280058	0	0.698344	0	0	0
CHIH	1206	−1	0.097854	0	0	0.141631	0	0.760515	0	0	0
POM	1190	0	0.038938	0	0	0.115044	0	0.846018	0	0	0
POM	1191	−2	0.480901	0	0	0.020568	0	0.498531	0	0	0
POM	1210	−7	0.020236	0	0	0.15683	0	0.822934	0	0	0
POM	1238	0	0.006961	0	0	0.226605	0	0.766435	0	0	0
POM	1239	−14	0.006266	0	0	0.373434	0	0.620301	0	0	0
DACH	1051	−5	0.008145	0	0	0.095023	0	0.896833	0	0	0
DACH	1052	−2	0.013889	0	0	0.007937	0	0.978175	0	0	0
DACH	1053	−1	0.009747	0	0	0.025341	0	0.964912	0	0	0
DACH	1054	0	0.006917	0	0	0.011858	0	0.981225	0	0	0
DACH	1055	−1	0.010848	0	0	0.013807	0	0.975345	0	0	0
BEAG	994	−2	0.004869	0	0	0.02629	0	0.968841	0	0	0
BEAG	995	−1	0.002681	0	0	0.106345	0	0.890974	0	0	0
BEAG	1323	−1	0.009747	0	0	0.025341	0	0.964912	0	0	0
BEAG	1324	0	0.002839	0	0	0.290277	0	0.706884	0	0	0
BEAG	1327	0	0.01256	0	0	0.033816	0	0.953623	0	0	0
IBIZ	1147	−8	0.011867	0	0	0.208861	0	0.779272	0	0	0
IBIZ	1148	−20	0.01225	0	0	0.355255	0	0.632495	0	0	0
IBIZ	1162	0	0.019639	0	0	0.214454	0	0.765907	0	0	0
IBIZ	1172	0	0.00639	0	0	0.201278	0	0.792332	0	0	0
IBIZ	1280	−1	0.023682	0	0	0.236058	0	0.74026	0	0	0
BMD	941	−11	0.009709	0	0	0.029126	0	0.961165	0	0	0
BMD	943	−10	0.006686	0	0	0.04489	0	0.948424	0	0	0
BMD	968	−17	0.005831	0	0	0.028183	0	0.965986	0	0	0
BMD	970	−31	0.011354	0	0	0.18897	0	0.799676	0	0	0
BMD	971	−51	0.020568	0	0	0.020568	0	0.958864	0	0	0
NEWF	271	−3	0.010913	0	0	0.007937	0	0.981151	0	0	0
NEWF	274	−1	0.019881	0	0	0.005964	0	0.974155	0	0	0
NEWF	275	−3	0.010934	0	0	0.005964	0	0.983101	0	0	0
NEWF	277	0	0.05859	0	0	0.006951	0	0.934459	0	0	0
NEWF	278	−1	0.034213	0	0	0.022483	0	0.943304	0	0	0
ROTT	1014	−2	0.0059	0	0	0.016716	0	0.977384	0	0	0
ROTT	1028	−3	0.005946	0	0	0.00892	0	0.985134	0	0	0
ROTT	1029	−1	0.004955	0	0	0.00892	0	0.986125	0	0	0
ROTT	1033	−1	0.009728	0	0	0.027237	0	0.963035	0	0	0
ROTT	1034	0	0.021782	0	0	0.009901	0	0.968317	0	0	0
PRES	1082	−3	0.419635	0	0	0.13119	0	0.449175	0	0	0
PRES	1093	−14	0.430979	0	0	0.197432	0	0.371589	0	0	0
PRES	1096	0	0.705253	0	0	0.027237	0	0.26751	0	0	0
PRES	1115	−1	0.572519	0	0	0.045802	0	0.381679	0	0	0
PRES	1127	−7	0.418004	0	0	0.108734	0	0.473262	0	0	0
BOX	1176	−1	0.002964	0	0	0.004941	0	0.006917	0.985178	0	0

TABLE 15D-continued

Canid Population[a]	Canid ID No.	Missing Data	Groups 1	2	3	4	5	6	7	8	9
BOX	1177	0	0.046332	0	0	0.002896	0	0.031853	0.918919	0	0
BOX	1178	−1	0.002979	0	0	0.003972	0	0.002979	0.99007	0	0
BOX	1179	−3	0.000993	0	0	0.003972	0	0.002979	0.992056	0	0
BOX	1304	−1	0.001978	0	0	0.005935	0	0.004946	0.987141	0	0
BULD	1193	−1	0.001938	0	0	0.006783	0	0.021318	0.002907	0.967054	0
BULD	1194	−2	0.004931	0	0	0.003945	0	0.006903	0.002959	0.981262	0
BULD	1195	−9	0.000988	0	0	0.004941	0	0.004941	0.001976	0.987154	0
BULD	1197	−3	0.003552	0	0	0.019538	0	0.089698	0.002664	0.884547	0
BULD	1198	0	0.003918	0	0	0.002938	0	0.013712	0.003918	0.975514	0
MAST	991	−14	0.984143	0	0	0	0	0.005946	0.000991	0.001982	0.006938
MAST	1015	0	0.979331	0	0	0	0	0.011811	0.001969	0.001969	0.004921
MAST	1016	−1	0.978389	0	0	0	0	0.008841	0.000982	0.007859	0.003929
MAST	1017	−22	0.966926	0	0	0	0	0.024319	0.000973	0.001946	0.005837
MAST	1066	−2	0.982266	0	0	0	0	0.006897	0.00197	0.005911	0.002956
BULM	1105	0	0.003925	0	0	0	0	0.009814	0.003925	0.004907	0.977429
BULM	1106	−3	0.002935	0	0	0	0	0.013699	0.001957	0.005871	0.975538
BULM	1107	−1	0.003956	0	0	0	0	0.006924	0.001978	6.001978	0.985163
BULM	1108	0	0.009852	0	0	0	0	0.010837	0.000985	0.002956	0.975369
BULM	1109	0	0.003956	0	0	0	0	0.004946	0.002967	0.002967	0.985163

[a] See Table 5 for abbreviations of canid populations.

KBB: pbe

TABLE 16

Average Membership Coefficient for Each Breed
From the K = 4 Cluster Results

Breed	Number of Individuals	Inferred Clusters 1	2	3	4
Shiba Inu	5	0.974	0.007	0.010	0.009
Chow Chow	5	0.983	0.006	0.005	0.006
Akita	5	0.977	0.005	0.013	0.006
Alaskan Malamute	5	0.884	0.029	0.023	0.064
Basenji	5	0.925	0.030	0.012	0.033
Chinese Shar-Pei	5	0.894	0.050	0.029	0.027
Siberian Husky	5	0.828	0.021	0.071	0.080
Afghan Hound	5	0.634	0.041	0.068	0.256
Saluki	5	0.392	0.041	0.058	0.509
Tibetan Terrier	5	0.368	0.120	0.141	0.371
Lhasa Apso	5	0.402	0.030	0.444	0.125
Samoyed	5	0.404	0.017	0.501	0.078
Pekingese	5	0.210	0.026	0.603	0.161
Shih Tzu	5	0.199	0.026	0.616	0.159
Irish Wolfhound	5	0.011	0.165	0.650	0.173
Saint Bernard	5	0.016	0.201	0.557	0.226
Greyhound	5	0.017	0.091	0.740	0.152
Belgian Sheepdog	5	0.013	0.009	0.962	0.016
Belgian Tervuren	4	0.018	0.022	0.856	0.103
Borzoi	5	0.041	0.024	0.720	0.215
Collie	5	0.007	0.019	0.766	0.208
Shetland Sheepdog	5	0.017	0.105	0.684	0.193
Pug Dog	5	0.022	0.017	0.466	0.494
Komondor	5	0.039	0.101	0.206	0.653
Whippet	5	0.007	0.087	0.480	0.426
Standard Poodle	5	0.032	0.144	0.370	0.454
Bichon Frise	4	0.074	0.087	0.362	0.477
Keeshond	5	0.016	0.043	0.479	0.462
Manchester Terrier, Toy	4	0.024	0.161	0.303	0.513
Norwegian Elkhound	5	0.104	0.090	0.329	0.477
Kuvasz	5	0.077	0.043	0.378	0.502
Great Dane	5	0.067	0.085	0.240	0.608
Welsh Springer Spaniel	5	0.007	0.083	0.255	0.654
Doberman Pinscher	5	0.015	0.103	0.194	0.688
Standard Schnauzer	5	0.006	0.149	0.165	0.681
Italian Greyhound	5	0.074	0.068	0.096	0.762
Old English Sheepdog	5	0.024	0.086	0.122	0.768
American Water Spaniel	5	0.023	0.127	0.131	0.719
Miniature Schnauzer	5	0.009	0.136	0.129	0.726
Australian Terrier	5	0.022	0.107	0.104	0.767
English Cocker Spaniel	5	0.004	0.088	0.182	0.725
Irish Setter	5	0.005	0.074	0.117	0.804
West Highland White Terrier	5	0.019	0.079	0.058	0.844
Pointer	5	0.019	0.067	0.105	0.809
Basset Hound	4	0.020	0.086	0.077	0.818
Cavalier King Charles Spaniel	5	0.013	0.078	0.122	0.787
Giant Schnauzer	5	0.106	0.082	0.060	0.752
Pharaoh Hound	4	0.102	0.081	0.025	0.792
Golden Retriever	5	0.009	0.184	0.019	0.789
Beagle	5	0.016	0.175	0.058	0.751
Bloodhound	5	0.009	0.203	0.014	0.775
Airedale Terrier	4	0.016	0.127	0.109	0.748
American Cocker Spaniel	5	0.010	0.103	0.053	0.834
American Hairless Rat Terrier	5	0.009	0.149	0.064	0.778
Chesapeake Bay Retriever	5	0.019	0.173	0.032	0.776
Cairn Terrier	5	0.015	0.123	0.073	0.790
Portuguese Water Dog	5	0.007	0.134	0.139	0.720
German Shorthaired Pointer	5	0.015	0.172	0.094	0.719
Border Collie	5	0.037	0.116	0.101	0.746
Bedlington Terrier	4	0.010	0.233	0.145	0.613
Clumber Spaniel	5	0.005	0.355	0.066	0.573
Ibizan Hound	5	0.015	0.149	0.120	0.716
Rhodesian Ridgeback	5	0.010	0.215	0.150	0.625
Dachshund	5	0.015	0.315	0.192	0.479
Australian Shepherd	5	0.068	0.221	0.170	0.540
Chihuahua	5	0.028	0.229	0.161	0.582
Kerry Blue Terrier	5	0.008	0.257	0.147	0.588
Schipperke	4	0.011	0.195	0.078	0.717
Irish Terrier	4	0.009	0.277	0.070	0.644
Flat-coated Retriever	5	0.005	0.207	0.084	0.704
Soft Coated Wheaten Terrier	4	0.035	0.329	0.163	0.473
Pomeranian	5	0.055	0.340	0.203	0.402
Labrador Retriever	5	0.033	0.488	0.075	0.404
Presa Canario	5	0.036	0.762	0.044	0.158
Rottweiler	5	0.006	0.798	0.098	0.098
Bullmastiff	5	0.008	0.873	0.032	0.087

TABLE 16-continued

Average Membership Coefficient for Each Breed From the K = 4 Cluster Results

Breed	Number of Individuals	Inferred Clusters 1	2	3	4
Newfoundland	5	0.020	0.923	0.018	0.040
German Shepherd Dog	5	0.006	0.858	0.090	0.046
French Bulldog	4	0.009	0.945	0.012	0.034
Miniature Bull Terrier	5	0.013	0.921	0.020	0.047
Bulldog	5	0.008	0.962	0.019	0.011
Boxer	5	0.003	0.923	0.065	0.008
Mastiff	5	0.010	0.934	0.032	0.024
Bernese Mountain Dog	5	0.006	0.708	0.229	0.057
Greater Swiss Mountain Dog	5	0.015	0.488	0.373	0.124

TABLE 17A

Canid Population^a	Canid ID No.	Missing Data	Populations* 1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21
CHOW	1633	−10	0.006	0.001	0.001	0.002	0.001	0.023	0.003	0.002	0.001	0.001	0.001	0.001	0.001	0.915	0.002	0.004	0.002	0.021	0.006	0.002	0.003
CHOW	1835	−9	0.001	0.001	0.001	0.001	0.002	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.981	0.001	0.001	0.003	0.001	0.001	0.001	0.001
CHOW	1837	−18	0.001	0.001	0.001	0.001	0.003	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0	0.981	0.001	0.001	0.001	0.001	0	0.001	0.001
CHOW	1838	−19	0.001	0.001	0.005	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0	0.001	0.978	0.001	0.001	0	0.002	0.001	0.001	0.001
CHOW	1839	−1	0.002	0.001	0.001	0.001	0.003	0.013	0.016	0.001	0.001	0.001	0.001	0.001	0.002	0.936	0.004	0.001	0.001	0.009	0.003	0.001	0.002
SHAR	1573	−5	0.001	0.001	0.001	0.002	0.002	0.964	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.002	0.001	0.003	0.012	0.001	0.002	0.001	0.001
SHAR	1593	−11	0.011	0.001	0.001	0.002	0.003	0.935	0.002	0.001	0.002	0.001	0.008	0.002	0.001	0.009	0.002	0.003	0.002	0.006	0.001	0.005	0.006
SHAR	1619	−6	0.001	0.001	0.001	0.001	0.001	0.982	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.002	0.001
SHAR	1998	−2	0.016	0.025	0.001	0.002	0.043	0.72	0.003	0.002	0.005	0.01	0.006	0.004	0.003	0.049	0.003	0.003	0.002	0.003	0.001	0.094	0.005
SHAR	1999	−4	0.031	0	0.002	0.004	0.098	0.713	0.062	0.003	0.002	0.003	0.001	0.004	0.004	0.025	0.001	0.01	0.004	0.002	0.001	0.001	0.026
SHIB	1769	−22	0.001	0.001	0.001	0.001	0.003	0.001	0.002	0.001	0.001	0.001	0.001	0.001	0.001	0.002	0.001	0.001	0.98	0.001	0	0.001	0.001
SHIB	1854	−11	0.002	0.001	0.001	0.001	0.008	0.002	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.006	0.002	0.001	0.958	0.001	0.011	0.001	0.001
SHIB	1856	−6	0.003	0.001	0.001	0.003	0.001	0.035	0.002	0.002	0.004	0.002	0.001	0.005	0.001	0.021	0.001	0.013	0.837	0.002	0.001	0.001	0.064
SHIB	1860	−7	0.002	0.001	0.001	0.001	0.01	0.008	0.001	0.001	0.002	0.001	0.001	0.001	0.001	0.005	0.001	0.002	0.958	0.001	0.001	0.001	0.002
SHIB	1981	−1	0.004	0.001	0.002	0.001	0.026	0.01	0.001	0.002	0.001	0.002	0.005	0.006	0.001	0.053	0.001	0.003	0.875	0.001	0.002	0.001	0.003
AKIT	1130	−5	0.002	0.001	0.001	0.001	0.969	0.001	0.002	0.001	0.001	0.001	0.007	0.001	0	0.001	0.001	0.001	0.005	0.001	0.001	0.001	0.001
AKIT	1131	0	0.003	0.001	0.001	0.002	0.97	0.001	0.001	0.003	0.003	0.001	0.001	0	0.001	0.005	0.001	0.001	0.002	0.001	0	0.001	0.001
AKIT	1132	−3	0.001	0	0.001	0.001	0.981	0.002	0.003	0.001	0.001	0.001	0	0.001	0.001	0.002	0.001	0.001	0.001	0.001	0	0.001	0.001
AKIT	1133	−5	0.002	0.001	0.001	0	0.974	0.003	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.003	0.001	0.001	0.003	0.002	0	0.002	0.001
AKIT	1134	−3	0.001	0.001	0.004	0.001	0.976	0.002	0.001	0.001	0.002	0.001	0.001	0.001	0.001	0.002	0.001	0.001	0.002	0.001	0.001	0.001	0.001
AMAL	1629	−3	0.003	0.002	0.001	0.015	0	0.002	0.952	0.001	0.001	0.002	0.002	0.003	0.001	0.003	0.001	0.002	0.002	0.002	0.001	0.001	0.002
AMAL	1779	−3	0.002	0.005	0.003	0.004	0.001	0.002	0.938	0.001	0.002	0.003	0.012	0.001	0.002	0.001	0.002	0.004	0.001	0.001	0.001	0.004	0.008
AMAL	1845	−3	0.003	0.003	0.003	0.001	0.003	0.002	0.964	0.001	0.001	0.002	0.004	0.001	0.004	0.001	0.001	0.001	0.001	0.002	0.001	0.001	0.001
AMAL	2132	−6	0.005	0.004	0.002	0.001	0.003	0.001	0.925	0.01	0.002	0.008	0.013	0.001	0.003	0.001	0.001	0.001	0.002	0.002	0.001	0.011	0.004
AMAL	2214	−1	0.003	0.002	0.01	0.004	0.004	0.001	0.943	0.004	0.001	0.002	0.001	0.007	0.001	0.001	0.001	0.002	0.004	0.001	0.001	0.003	0.002
HUSK	1469	−12	0.002	0.001	0.001	0.001	0.001	0.001	0.96	0.001	0.008	0.002	0.001	0.001	0.001	0.013	0.001	0.001	0.001	0.001	0.001	0.001	0.002
HUSK	1883	−2	0.002	0.001	0.011	0.001	0.001	0.001	0.956	0.003	0.003	0.001	0.001	0.001	0.001	0.003	0.002	0.001	0.001	0.002	0.001	0.005	0.002
HUSK	2115	−6	0.003	0.001	0.001	0.006	0.001	0.002	0.947	0.004	0.002	0.003	0.004	0.004	0.002	0.001	0.005	0.003	0.001	0.001	0.001	0.002	0.007
HUSK	2117	−1	0.019	0.041	0.002	0.001	0.002	0.002	0.778	0.007	0.003	0.003	0.002	0.001	0.002	0.009	0.002	0.004	0.002	0.003	0.001	0.11	0.006
HUSK	2118	−3	0.013	0.001	0.004	0.031	0.001	0.003	0.838	0.025	0.001	0.003	0.004	0.003	0.002	0.003	0.001	0.016	0.002	0.004	0.014	0.027	0.005
SAMO	1375	0	0.001	0.001	0.961	0.002	0.001	0.001	0.001	0.001	0.008	0.001	0.001	0.008	0.001	0.001	0.001	0.001	0.001	0.002	0.001	0.004	0.001
SAMO	1532	−5	0.001	0.001	0.973	0.001	0.001	0.001	0.002	0.001	0.001	0.001	0.001	0.001	0.003	0.001	0.001	0.002	0.002	0.001	0.001	0.003	0.001
SAMO	1560	−1	0.002	0.007	0.928	0.001	0.001	0.003	0.001	0.017	0.003	0.011	0.002	0.001	0.001	0.001	0.001	0.009	0.001	0.002	0.002	0.002	0.007
SAMO	169	0	0.001	0.001	0.981	0.001	0.001	0.001	0.001	0.002	0.001	0.001	0.002	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001
SAMO	239	0	0.002	0.002	0.97	0.002	0.002	0.001	0.001	0.001	0.002	0.001	0.003	0.003	0	0.001	0.001	0.002	0.001	0.002	0.002	0.001	0.001
AFGH	1812	−3	0.002	0.001	0.001	0.002	0.001	0.001	0.003	0.001	0.001	0.001	0.001	0.001	0.976	0.001	0.002	0.001	0.001	0.001	0.002	0.001	0.001
AFGH	1939	−3	0.001	0.002	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.981	0	0.002	0.001	0.001	0.001	0.001	0.001	0.001
AFGH	2264	−7	0.001	0.001	0.001	0.001	0	0.001	0.001	0.001	0.001	0.001	0.002	0.001	0.983	0	0.001	0.001	0	0.001	0.001	0.001	0.001
AFGH	1936	−9	0.001	0.001	0.001	0.001	0	0.001	0.001	0.001	0.001	0.001	0.001	0	0.983	0.001	0.001	0.001	0	0.001	0.001	0.001	0.001
AFGH	1937	−13	0.002	0.001	0.006	0.005	0.001	0.001	0.007	0.002	0.002	0.002	0.002	0.002	0.948	0.001	0.004	0.003	0	0.001	0	0.001	0.009
SALU	1491	0	0.004	0.001	0.001	0.002	0.001	0.001	0.001	0.01	0.002	0.001	0.003	0.001	0.02	0.001	0.922	0.002	0.004	0.009	0.001	0.009	0.002
SALU	1535	−5	0.002	0.002	0.002	0.001	0.001	0.001	0.019	0.001	0.002	0.002	0.003	0.001	0.02	0.002	0.931	0.001	0.001	0.002	0.002	0.001	0.002
SALU	1607	−14	0.001	0.001	0.002	0.001	0.001	0.001	0.002	0.001	0.001	0.001	0.002	0.002	0.017	0.001	0.961	0.001	0.001	0.001	0.001	0.002	0.001
SALU	1873	−2	0.001	0.001	0.001	0.002	0.001	0.006	0.002	0.002	0.001	0.007	0.005	0.004	0.019	0.001	0.939	0.002	0.001	0.001	0.001	0.001	0.002
SALU	2610	−20	0.078	0.004	0.001	0.011	0.003	0.005	0.005	0.1	0.002	0.007	0.004	0.004	0.075	0.005	0.579	0.032	0.001	0.001	0.032	0.006	0.046
BSJI	1338	−9	0.281	0.001	0.001	0.002	0.005	0.003	0.001	0.002	0.001	0.026	0.002	0.003	0.002	0.001	0.017	0.03	0.004	0.002	0.548	0.003	0.064
BSJI	1339	−3	0.001	0.002	0.001	0.001	0.001	0.001	0.001	0.001	0	0	0.001	0.001	0.001	0.001	0	0.001	0	0.001	0.986	0.001	0.001

TABLE 17A-continued

Canid Population^a	Canid ID No.	Missing Data	Populations*																				
			1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21
BSJI	1645	−12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.992	0	0
BSJI	1675	0	0.001	0.001	0.001	0.001	0	0.001	0.001	0.001	0.001	0	0.001	0	0	0	0.001	0.001	0.001	0.001	0.988	0	0.001
BSJI	1717	−2	0.002	0	0.001	0.001	0.001	0.001	0.001	0.001	0	0.001	0.001	0.001	0.004	0.001	0.001	0	0.005	0.001	0.976	0.001	0.001
TIBT	1466	−8	0.006	0.003	0.005	0.003	0.005	0.002	0.003	0.014	0.002	0.009	0.007	0.008	0.004	0.002	0.004	0.003	0.004	0.904	0.002	0.005	0.005
TIBT	1562	−9	0.001	0.001	0.001	0.001	0	0	0.001	0.001	0.001	0.001	0.001	0.001	0	0.001	0	0.002	0.001	0.985	0.001	0.001	0.001
TIBT	1707	−12	0.001	0.01	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.002	0.001	0.002	0.001	0.001	0.001	0.001	0	0.974	0	0.001	0.001
TIBT	26078	−2	0.012	0.004	0.004	0.003	0.005	0.002	0.006	0.008	0.023	0.076	0.009	0.004	0.003	0.002	0.031	0.009	0.015	0.756	0.001	0.001	0.027
TIBT	28086	0	0.001	0.001	0.001	0.001	0	0.001	0.001	0.004	0	0.001	0.001	0.002	0.001	0.001	0.001	0.001	0.001	0.967	0.001	0.012	0.001
LHSA	1524	−1	0.002	0.002	0.002	0.086	0.001	0.001	0.002	0.001	0.081	0.005	0.002	0.001	0.001	0.001	0.001	0.269	0.003	0.001	0.001	0.003	0.537
LHSA	1525	−41	0.003	0.002	0.004	0.043	0.001	0.002	0.002	0.002	0.245	0.003	0.002	0.001	0.003	0.002	0.002	0.138	0.002	0.001	0.003	0.004	0.535
LHSA	1526	−18	0.006	0.001	0.005	0.085	0.001	0.002	0.001	0.002	0.007	0.003	0.004	0.005	0.004	0.001	0.002	0.22	0.001	0.001	0.001	0.002	0.647
LHSA	1528	−2	0.003	0.002	0.004	0.051	0.001	0.001	0.004	0.238	0.166	0.004	0.001	0.009	0.001	0.006	0.01	0.157	0.001	0.009	0.002	0.003	0.325
LHSA	2074	−3	0.004	0.002	0.001	0.079	0.001	0.001	0.004	0.004	0.009	0.001	0.001	0.002	0.001	0.001	0.005	0.203	0.002	0.003	0.002	0.001	0.672
PEKE	1143	0	0	0.001	0	0.001	0	0	0.001	0	0.99	0.001	0	0	0	0.001	0	0.001	0	0	0	0	0.001
PEKE	1145	−2	0.001	0.002	0.001	0.004	0.001	0.001	0.001	0.001	0.974	0.001	0.001	0.001	0.001	0.002	0.002	0.002	0.001	0.001	0.001	0.001	0.001
PEKE	1211	0	0.001	0.001	0.001	0.005	0.001	0.002	0.001	0.002	0.951	0.001	0.003	0.002	0.001	0.001	0.001	0.023	0	0.001	0.001	0.001	0.002
PEKE	1212	−1	0.003	0.012	0.002	0.008	0.001	0.001	0.001	0.002	0.919	0.001	0.004	0.001	0.002	0.001	0.006	0.026	0.001	0.001	0.004	0.002	0.003
PEKE	1213	−3	0.001	0.014	0.001	0.001	0.001	0.001	0.001	0.001	0.963	0.002	0.002	0.001	0.001	0.001	0.001	0.002	0.001	0.001	0.001	0.001	0.003
SHIH	1393	0	0.001	0.001	0.001	0.166	0.001	0.002	0.001	0.001	0.106	0.001	0.001	0.002	0	0.001	0.001	0.71	0.001	0.001	0	0.001	0.001
SHIH	1783	−11	0.001	0.002	0.001	0.186	0.001	0.001	0.001	0.006	0.018	0.001	0.001	0.002	0.001	0.001	0.001	0.769	0.001	0.001	0.001	0.002	0.005
SHIH	2068	−3	0.001	0.001	0.001	0.188	0.001	0.001	0.001	0.001	0.021	0.001	0.001	0.001	0.001	0.001	0.001	0.772	0.001	0.001	0	0.001	0.005
SHIH	2859	−44	0.001	0.001	0.001	0.198	0.002	0.002	0.001	0.001	0.002	0.001	0.002	0.001	0.001	0.002	0.001	0.777	0.002	0.001	0.001	0.001	0.001
SHIH	2860	−12	0.002	0.002	0.001	0.151	0.007	0.001	0.001	0.002	0.124	0.001	0.001	0.003	0.001	0.005	0.001	0.624	0.005	0.001	0.001	0.001	0.068
PUG	1077	−5	0.001	0.986	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0	0	0.001	0.001	0.001	0.001	0	0.001	0.001
PUG	1104	0	0.001	0.954	0.001	0.004	0.001	0.001	0.002	0.001	0.005	0.004	0.001	0.001	0.001	0.001	0.001	0.014	0.001	0.003	0.001	0.001	0.002
PUG	1183	−2	0.001	0.986	0.001	0.001	0.002	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0	0.001	0.001	0.001	0	0.001	0.001	0.001	0.001
PUG	1184	−1	0	0.993	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
PUG	1192	−3	0.001	0.986	0.001	0.001	0.001	0	0.001	0.001	0	0.001	0.001	0.001	0.001	0.001	0.001	0	0	0.001	0	0.001	0.001
BICH	1943	−17	0.002	0.002	0.007	0.003	0.007	0.002	0.002	0.917	0.002	0.007	0.003	0.003	0.001	0.003	0.001	0.003	0.001	0.023	0.001	0.008	0.004
BICH	1954	−7	0.002	0.001	0.001	0.004	0	0.001	0.001	0.963	0.001	0.001	0.001	0.003	0.002	0.001	0.005	0.004	0.003	0.003	0.001	0.002	0.001
BICH	933	−4	0.002	0.002	0.003	0.001	0.001	0.002	0.001	0.954	0.001	0.003	0.001	0.004	0.004	0.001	0.003	0.003	0.001	0.006	0.001	0.002	0.005
BICH	974	−2	0.002	0.091	0.002	0.001	0.001	0.002	0.003	0.87	0.002	0.001	0.005	0.002	0.001	0.001	0.001	0.004	0.001	0.001	0.002	0.005	0.002
SPOO	1530	−3	0.004	0.001	0.003	0.003	0.001	0.002	0.005	0.006	0.001	0.003	0.002	0.942	0.001	0.002	0.004	0.002	0.002	0.011	0.001	0.003	0.003
SPOO	1582	−1	0.002	0.001	0.002	0.004	0.001	0.002	0.001	0.003	0.001	0.003	0.001	0.954	0.001	0.001	0.001	0.003	0.001	0.001	0.004	0.005	0.006
SPOO	1876	−18	0.01	0.001	0.003	0.054	0.001	0.002	0.002	0.005	0.001	0.012	0.003	0.818	0.003	0.001	0.004	0.047	0.001	0.002	0.003	0.022	0.006
SPOO	1877	−5	0.002	0.001	0.002	0.002	0.001	0.001	0.001	0.002	0.002	0.009	0.001	0.964	0.002	0.001	0.004	0.001	0.002	0.001	0.001	0.001	0.002

TABLE 17A-continued

			Populations*																				
Canid Population[a]	Canid ID No.	Missing Data	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21
SPOO	2337	−13	0.001	0.002	0.001	0.003	0.001	0.001	0.001	0.002	0.001	0.002	0.002	0.961	0.004	0.001	0.001	0.002	0.001	0.007	0.001	0.002	0.001
KOMO	1484	−13	0.001	0.001	0.003	0.001	0.001	0.001	0.003	0.001	0.002	0.967	0.002	0.002	0.001	0.001	0.002	0.001	0.001	0.004	0.001	0.003	0.002
KOMO	1964	−17	0.014	0.001	0.001	0.003	0.001	0.001	0.001	0.003	0.001	0.851	0.025	0.007	0.011	0.002	0.047	0.002	0.002	0.003	0.003	0.014	0.007
KOMO	2321	−1	0.002	0.017	0.002	0.012	0.001	0.001	0.003	0.019	0.001	0.899	0.001	0.003	0.002	0.001	0.001	0.005	0.001	0.008	0.001	0.021	0.002
KOMO	2323	−1	0.004	0.014	0.003	0.003	0.001	0.002	0.001	0.002	0.009	0.859	0.002	0.083	0.004	0.001	0.001	0.004	0.001	0.002	0.001	0.001	0.003
KOMO	2334	−2	0.001	0.004	0.002	0.002	0.002	0.001	0.001	0.002	0.003	0.968	0.002	0.001	0.002	0.001	0.001	0.001	0.001	0.001	0.001	0.003	0.001
KUVZ	1482	−3	0.002	0.009	0.013	0.047	0.001	0.001	0.006	0.009	0.001	0.002	0.001	0.006	0.001	0.001	0.004	0.004	0	0.001	0.001	0.889	0.001
KUVZ	1551	0	0.004	0.001	0.002	0.002	0.001	0.003	0.002	0.015	0.001	0.001	0.013	0.027	0.001	0.001	0.005	0.002	0.002	0.007	0.002	0.905	0.003
KUVZ	1672	−23	0.002	0.004	0.001	0.005	0.011	0.001	0.002	0.001	0.001	0.007	0.001	0.007	0.002	0.001	0.001	0.002	0.001	0.001	0.001	0.942	0.003
KUVZ	1913	−2	0.004	0.001	0.006	0.007	0.001	0.003	0.002	0.007	0.004	0.01	0.012	0.003	0.026	0.001	0.003	0.005	0.001	0.003	0.001	0.896	0.003
KUVZ	1994	−2	0.005	0.002	0.006	0.003	0.001	0.003	0.001	0.006	0.003	0.008	0.005	0.014	0.002	0.002	0.002	0.003	0.001	0.003	0.006	0.916	0.006
KEES	1501	0	0.001	0.003	0.188	0.771	0.001	0.001	0.003	0.002	0.001	0.001	0.008	0.003	0.002	0.001	0.002	0.004	0.001	0.002	0.004	0.002	0.001
KEES	1589	−2	0.002	0.008	0.155	0.77	0.001	0.002	0.001	0.002	0.002	0.004	0.017	0.003	0.003	0.001	0.021	0.002	0.001	0.001	0.001	0.002	0.002
KEES	1818	−41	0.001	0.001	0.19	0.778	0.001	0.001	0.001	0.001	0.001	0.002	0.004	0.006	0.001	0.001	0.002	0.001	0.001	0.002	0.001	0.001	0.001
KEES	1819	−1	0.002	0.002	0.174	0.767	0.002	0.001	0.001	0.02	0.001	0.002	0.002	0.009	0.001	0.001	0.001	0.002	0.001	0.003	0.002	0.004	0.002
KEES	2072	−4	0.003	0.003	0.168	0.749	0.001	0.001	0.002	0.035	0.005	0.003	0.001	0.008	0.002	0.001	0.002	0.002	0.001	0.001	0.002	0.006	0.004
NELK	2216	−4	0.039	0.003	0.018	0.017	0.001	0.002	0.005	0.004	0.003	0.008	0.846	0.005	0.002	0.01	0.002	0.006	0.001	0.011	0.004	0.004	0.01
NELK	2239	−2	0.001	0.001	0.001	0.002	0	0.001	0.001	0.001	0.001	0.001	0.984	0.001	0	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001
NELK	2240	−2	0.002	0.001	0.005	0.008	0.001	0.001	0.002	0.002	0.007	0.003	0.948	0.002	0.001	0.001	0.003	0.002	0.001	0.002	0.001	0.008	0.001
NELK	2281	−1	0.001	0.003	0.002	0.008	0.001	0.001	0.002	0.002	0.001	0.001	0.949	0.001	0.005	0.001	0.008	0.001	0.001	0.01	0.001	0.001	0.001
NELK	2295	−15	0.001	0.002	0.002	0.002	0.002	0.001	0.002	0.002	0.001	0.001	0.957	0.001	0.001	0.001	0.004	0.004	0.001	0.007	0.001	0.003	0.002

TABLE 17B

			Populations*																				
Canid Population[a]	Canid ID No.	Missing Data	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64
ECKR	1376	−1	0.002	0.001	0.01	0.002	0.003	0.001	0.863	0.007	0.001	0.001	0.002	0.008	0.001	0.001	0.001	0.006	0.003	0.004	0.002	0.072	0.009
ECKR	1377	−2	0.001	0.056	0.012	0.003	0.003	0.002	0.859	0.001	0.007	0.001	0.004	0.003	0.003	0.002	0.002	0.003	0.003	0.005	0.003	0.023	0.002
ECKR	1400	−2	0.001	0.001	0	0.001	0.001	0.001	0.983	0.002	0.001	0.001	0.001	0.001	0.001	0	0.001	0.001	0.001	0	0.001	0.002	0
ECKR	1404	−7	0.001	0.001	0.002	0.001	0.001	0.001	0.977	0.001	0.001	0.001	0.001	0.001	0.002	0.001	0.003	0.001	0.001	0.001	0.001	0.001	0.001
ECKR	1511	−6	0.002	0.004	0.003	0.001	0.001	0.001	0.959	0.001	0.001	0.002	0.004	0.001	0.001	0.005	0.003	0.001	0.002	0.002	0.004	0.002	0.001
ACKR	1035	−2	0.002	0.001	0.001	0.739	0.003	0.186	0.009	0.001	0.003	0.002	0.001	0.007	0.003	0.023	0.001	0.001	0.007	0.002	0.003	0.004	0.001
ACKR	2261	−2	0.003	0.001	0.001	0.961	0.001	0.001	0.006	0.003	0.001	0.001	0.001	0.001	0.003	0.001	0.001	0.003	0.001	0.001	0.001	0.006	0.001
ACKR	2310	−1	0.004	0.001	0.001	0.949	0.019	0.003	0.002	0.004	0.001	0.001	0.001	0.002	0.001	0.001	0.002	0.001	0.002	0.001	0.002	0.001	0.001
ACKR	1956	−18	0.001	0.001	0.001	0.981	0.001	0.001	0.002	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.002	0.001	0.001	0.001	0.001	0.001	0.002
ACKR	2260	−2	0.001	0.001	0.001	0.983	0.001	0.001	0.002	0	0.001	0.001	0.001	0.001	0.001	0.002	0.001	0.001	0.001	0.001	0.001	0	0.001
CKCS	1513	−6	0.001	0.004	0.001	0.001	0.002	0.002	0.002	0.965	0.001	0.001	0.002	0.004	0.003	0.001	0.001	0.001	0.001	0.003	0.002	0.001	0.001
CKCS	1639	−2	0.001	0.003	0.001	0.001	0.001	0.001	0.001	0.98	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.002	0.001	0.002	0.001	0.001
CKCS	1640	−15	0.001	0.001	0.034	0	0.001	0.001	0.001	0.941	0.002	0.001	0.006	0.001	0.001	0.001	0.001	0.001	0.001	0.003	0.001	0.001	0.001
CKCS	1642	−4	0.005	0.001	0.001	0.003	0.001	0.001	0.002	0.975	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001
CKCS	2054	−5	0.001	0.001	0	0	0	0	0	0.991	0	0	0	0	0	0.001	0.001	0	0	0	0	0	0
DOBP	1031	−1	0.002	0.001	0.004	0.002	0.001	0.001	0.001	0.002	0.001	0.003	0.002	0.003	0.001	0.966	0.001	0.001	0.001	0.002	0.003	0.001	0.001
DOBP	1032	−3	0.001	0.001	0.001	0.002	0.004	0.011	0.004	0.001	0.026	0.002	0.001	0.001	0.001	0.929	0.001	0.001	0.005	0.001	0.002	0.003	0.002
DOBP	1749	−2	0.001	0.001	0.001	0.002	0.001	0.001	0	0	0.002	0.001	0.002	0.001	0.001	0.979	0.002	0.001	0.001	0.001	0.001	0	0.002
DOBP	2162	−5	0.009	0.001	0.004	0.001	0.001	0.001	0.001	0.002	0.001	0.001	0.002	0.001	0.002	0.964	0.001	0.001	0.003	0.001	0.001	0.001	0.001
DOBP	2245	−2	0.001	0	0	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0	0	0.001	0.989	0.001	0	0	0	0	0.001	0.001
MNTY	1539	−1	0.924	0.003	0.001	0.013	0.001	0.007	0.002	0.003	0.002	0.003	0.008	0.001	0.001	0.006	0.007	0.001	0.005	0.001	0.001	0.007	0.003
MNTY	1732	−15	0.978	0.001	0.001	0.002	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.004	0.002	0.001	0.001	0.001	0.001	0.001	0.001
MNTY	2145	−19	0.983	0.001	0.002	0.002	0.001	0.001	0.002	0.001	0.001	0.001	0.001	0	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001
MNTY	2149	−47	0.945	0.002	0.002	0.003	0.001	0.001	0.014	0.001	0.002	0.001	0.002	0.003	0.008	0.002	0.001	0.001	0.001	0.001	0.001	0.004	0.003
IRSE	1540	−5	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.006	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.978
IRSE	1617	−4	0.001	0.001	0.001	0.001	0.001	0.001	0	0.001	0.001	0.002	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.983
IRSE	1896	0	0.002	0.003	0.004	0.008	0.002	0.001	0.003	0.001	0.002	0.002	0.002	0.015	0.001	0.001	0.002	0.002	0.004	0.001	0.002	0.002	0.94
IRSE	2084	−6	0.017	0.002	0.008	0.003	0.002	0.001	0.002	0.001	0.003	0.001	0.001	0.001	0.001	0.001	0.004	0.001	0.002	0.014	0.008	0.001	0.927
IRSE	2085	−17	0.002	0.001	0.001	0.002	0.001	0.002	0.015	0.006	0.005	0.002	0.001	0.001	0.003	0.001	0.005	0.004	0.002	0.003	0.001	0.005	0.936
PNTR	1382	0	0.001	0.002	0.001	0.001	0.002	0.008	0.001	0.001	0.004	0.002	0.001	0.965	0.001	0.001	0.001	0.001	0.001	0.001	0.002	0.001	0.003
PNTR	1383	−2	0.002	0.003	0.002	0.001	0.001	0.002	0.001	0.003	0.001	0.001	0.002	0.967	0.003	0.001	0.002	0.001	0.001	0.002	0.001	0.001	0.002
PNTR	1869	−2	0.001	0.003	0.003	0.005	0.006	0.002	0.001	0.001	0.001	0.001	0.008	0.942	0.003	0.001	0.002	0.004	0.001	0.011	0.001	0.001	0.002
PNTR	1938	−6	0.001	0.001	0.001	0.003	0.001	0.002	0.001	0.001	0.004	0.001	0.002	0.965	0.001	0.001	0.002	0.001	0.002	0.002	0.001	0.006	0.003
PNTR	1948	−31	0.004	0.001	0.005	0.002	0.001	0.002	0.003	0.027	0.002	0.001	0.001	0.933	0.003	0.002	0.001	0.003	0.002	0.002	0.002	0.003	0.002
GSHP	1628	−5	0.025	0.002	0.009	0.002	0.005	0.808	0.002	0.002	0.003	0.003	0.011	0.015	0.001	0.087	0.002	0.002	0.003	0.002	0.012	0.002	0.003
GSHP	1708	−22	0.001	0.001	0.002	0.002	0.002	0.929	0.001	0.001	0.002	0.001	0.002	0.005	0.003	0.001	0.042	0.001	0.001	0.001	0.002	0.001	0.001
GSHP	1710	−28	0.001	0.001	0.002	0.002	0.002	0.959	0.002	0.001	0.002	0.001	0.002	0.001	0.002	0.001	0.001	0.005	0.003	0.005	0.001	0.006	0.001
GSHP	1833	−26	0.335	0.013	0.008	0.155	0.003	0.146	0.003	0.002	0.013	0.002	0.001	0.072	0.001	0.001	0.01	0.044	0.025	0.067	0.095	0.001	0.003
GSHP	1892	−4	0.012	0.001	0.003	0.004	0.104	0.398	0.002	0.004	0.016	0.002	0.001	0.012	0.002	0.002	0.004	0.182	0.011	0.004	0.028	0.003	0.203
MSNZ	1587	−9	0.001	0.001	0.984	0.001	0.001	0.001	0.001	0.001	0.001	0	0.001	0.001	0.001	0	0.001	0.001	0.001	0.001	0.001	0.001	0.001
MSNZ	1756	−6	0.001	0.001	0.982	0.001	0.001	0.001	0.001	0.001	0.001	0	0.001	0.001	0.001	0.001	0	0.001	0.001	0.001	0.001	0.002	0.001
MSNZ	1851	−7	0.001	0.001	0.976	0.001	0.001	0.001	0.002	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.002	0.002	0.003	0.001	0.001	0.001	0.001
MSNZ	2034	−1	0.001	0.001	0.919	0.001	0.002	0.003	0.001	0.001	0.005	0.002	0.001	0.002	0.003	0.001	0.027	0.001	0.011	0.01	0.004	0.001	0.001
MSNZ	2613	−16	0.001	0.001	0.912	0.006	0.001	0.002	0.028	0.001	0.002	0.003	0.001	0.002	0.023	0.003	0.003	0.001	0.001	0.002	0.001	0.003	0.002
SSNZ	13352	0	0.001	0.001	0.001	0.001	0.001	0.002	0.002	0.001	0.001	0.001	0.001	0.002	0.002	0.001	0.968	0.004	0.002	0.002	0.001	0.001	0.003
SSNZ	1360	−3	0.008	0.003	0.075	0.004	0.001	0.002	0.005	0.009	0.01	0.001	0.003	0.001	0.002	0.002	0.855	0.002	0.006	0.001	0.004	0.005	0.001
SSNZ	1827	−9	0.001	0	0.001	0.001	0.001	0.001	0	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.988	0.001	0.001	0	0.001	0	0.001

TABLE 17B-continued

			Populations*																				
Canid Population^a	Canid ID No.	Missing Data	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64
SSNZ	20457	−1	0.001	0.001	0.001	0.002	0.001	0.002	0.001	0.001	0.001	0.002	0.001	0.002	0.002	0	0.97	0.001	0.002	0.001	0.001	0.001	0.004
SSNZ	22647	−3	0.001	0.001	0.002	0.001	0.001	0.001	0.001	0.005	0.001	0.001	0.001	0.001	0.001	0.001	0.976	0.001	0.001	0.001	0.001	0.001	0.001
GSNZ	1868	−6	0.009	0.003	0.002	0.01	0.14	0.006	0.002	0.006	0.597	0.01	0.003	0.015	0.012	0.005	0.035	0.012	0.007	0.008	0.106	0.004	0.008
GSNZ	22739	0	0.001	0.001	0.006	0.002	0.042	0.002	0.001	0.003	0.928	0.001	0.001	0.001	0.001	0.002	0.001	0.001	0.001	0.001	0.001	0.001	0.003
GSNZ	27093	0	0.003	0.005	0.002	0.001	0.002	0.002	0.003	0.003	0.948	0.002	0.006	0.002	0.001	0.001	0.002	0.001	0.004	0.008	0.001	0.002	0.002
GSNZ	27106	−1	0.001	0.009	0.001	0.002	0.002	0.001	0.008	0.001	0.863	0.002	0.001	0.004	0.001	0.002	0.093	0.002	0.002	0.001	0.001	0.001	0.003
GSNZ	33390	0	0.007	0.003	0.007	0.003	0.002	0.004	0.004	0.002	0.775	0.004	0.04	0.001	0.104	0.002	0.016	0.012	0.004	0.002	0.005	0.001	0.001
AHRT	1120	−1	0.001	0.002	0.001	0.001	0.002	0.001	0.001	0.001	0.001	0.001	0.001	0.002	0.001	0.001	0.002	0.977	0.001	0.002	0.001	0.001	0.001
AHRT	1121	−3	0.001	0.001	0.002	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.002	0.001	0	0.001	0.979	0.001	0.002	0.002	0.001	0.001
AHRT	1122	0	0.004	0.004	0.002	0.006	0.061	0.004	0.002	0.002	0.003	0.002	0.001	0.001	0.016	0.003	0.001	0.854	0.009	0.002	0.008	0.008	0.005
AHRT	1123	−1	0.001	0.001	0.002	0.003	0.003	0.03	0.002	0.003	0.004	0.001	0.023	0.001	0.004	0.003	0.003	0.888	0.004	0.011	0.004	0.007	0.002
AHRT	1124	−2	0.001	0	0.001	0.001	0.001	0.001	0.001	0	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.984	0.001	0.001	0.001	0.001	0.001
AIRT	1603	−3	0.001	0	0.001	0.001	0.001	0.001	0.001	0	0.001	0	0.99	0.001	0.001	0	0	0.001	0.001	0.001	0	0.001	0
AIRT	1604	−7	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.002	0.001	0.001	0.975	0.001	0.005	0.001	0.002	0.001	0.001	0.001	0.001	0.001	0.001
AIRT	1788	−2	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.981	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.002
AIRT	1875	−1	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.982	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001
BASS	1341	0	0.001	0.003	0.001	0.001	0.981	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001
BASS	1342	−5	0.001	0.001	0.003	0.001	0.966	0.002	0.006	0.001	0.002	0.001	0.001	0.001	0.001	0.001	0.001	0.004	0.001	0.001	0.001	0.003	0.001
BASS	1506	0	0.001	0.002	0.001	0.001	0.951	0.001	0.004	0.002	0.001	0.004	0.001	0.001	0.001	0.002	0.001	0.001	0.002	0.002	0.005	0.011	0.005
BASS	1917	−4	0.001	0.003	0.001	0.001	0.971	0.007	0.002	0.001	0.002	0.001	0.001	0.001	0.002	0.001	0	0.001	0.001	0.003	0.001	0.001	0.001
BEAG	1323	−2	0.001	0.059	0.011	0.019	0.002	0.002	0.002	0.001	0.002	0.002	0.001	0.001	0.017	0.001	0.001	0.007	0.004	0.859	0.003	0.002	0.002
BEAG	1324	−1	0.003	0.001	0.004	0.002	0.005	0.04	0.001	0.012	0.004	0.003	0.001	0.001	0.001	0.231	0.001	0.244	0.008	0.421	0.012	0.002	0.001
BEAG	1327	−2	0.003	0.017	0.002	0.002	0.003	0.006	0.002	0.001	0.003	0.002	0.002	0.002	0.011	0.001	0.001	0.002	0.007	0.928	0.002	0.001	0.001
BEAG	994	−3	0.002	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.002	0.001	0.001	0.001	0.001	0.001	0.98	0.001	0.001	0.001
BEAG	995	−2	0.001	0.001	0.001	0.001	0.001	0.001	0.002	0.002	0.001	0.002	0.001	0.001	0.002	0.001	0.002	0.001	0.001	0.972	0.001	0.001	0.002
BLDH	1186	0	0.001	0.989	0	0.001	0.001	0.001	0.001	0	0	0	0	0	0.001	0.001	0	0	0.001	0.001	0	0.001	0
BLDH	1223	−2	0.01	0.945	0.001	0.002	0.001	0.002	0.003	0.006	0.001	0.001	0.001	0.001	0.002	0.001	0.001	0.001	0.001	0.006	0.001	0.006	0.007
BLDH	1410	−8	0.001	0.978	0.001	0.001	0.001	0.002	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.002	0.001	0.001	0.001
BLDH	1942	−6	0.001	0.981	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.003	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001
BLDH	1957	0	0.001	0.973	0.001	0.001	0.002	0.001	0.001	0.001	0.001	0.002	0.001	0.001	0.003	0.001	0.001	0.001	0.001	0.002	0.003	0.001	0.001
IBIZ	1147	−8	0.001	0.002	0.003	0.001	0.001	0.001	0.017	0.001	0.002	0.097	0.002	0.001	0.01	0.001	0.003	0.001	0.002	0.008	0.84	0.002	0.002
IBIZ	1148	−19	0.002	0.001	0.011	0.001	0.003	0.002	0.002	0.001	0.002	0.109	0.004	0.001	0.002	0.001	0.001	0.002	0.002	0.001	0.852	0.001	0.001
IBIZ	1162	0	0.001	0.002	0.002	0.002	0.001	0.001	0.003	0.001	0.002	0.247	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.725	0.001	0.003

TABLE 17B-continued

			Populations*																				
Canid Population[a]	Canid ID No.	Missing Data	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64
IBIZ	1172	0	0.002	0.075	0.001	0.007	0.001	0.001	0.001	0.001	0.003	0.098	0.001	0.001	0.002	0.001	0.002	0.002	0.002	0.002	0.795	0.001	0.002
IBIZ	1280	0	0.002	0.001	0.001	0.003	0.004	0.005	0.004	0.001	0.001	0.102	0.007	0.005	0.001	0.001	0.001	0.003	0.004	0.001	0.85	0.002	0.002
PHAR	1292	−3	0.001	0.001	0.001	0.001	0.002	0.001	0.001	0.001	0.001	0.977	0.001	0.001	0.001	0.001	0.001	0.001	0.004	0.001	0.002	0.001	0.002
PHAR	1947	−14	0.001	0	0.002	0.001	0.001	0.009	0.001	0.001	0.006	0.968	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.002	0.002	0.001	0.001
PHAR	1962	−14	0.001	0.001	0.001	0.002	0.001	0.002	0.001	0.001	0.001	0.969	0	0.001	0.001	0.001	0.002	0.001	0.005	0.001	0.003	0.003	0.001
PHAR	1963	−10	0.002	0.001	0.001	0.001	0.008	0.001	0.002	0.001	0.001	0.956	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.003	0.001	0.016
PTWD	P142	−3	0.002	0.001	0.009	0.001	0.001	0.001	0.002	0.001	0.002	0.002	0.007	0.003	0.005	0.002	0.002	0.005	0.942	0.002	0.003	0.005	0.002
PTWD	P1	−6	0.001	0.008	0.003	0.001	0.002	0.002	0.001	0.001	0.002	0.001	0.001	0.001	0.001	0.001	0.023	0.002	0.929	0.002	0.002	0.015	0.002
PTWD	P238	−3	0.003	0.002	0.005	0.005	0.004	0.025	0.002	0.021	0.035	0.024	0.008	0.007	0.002	0.002	0.003	0.003	0.503	0.301	0.018	0.022	0.005
PTWD	P25	−2	0.006	0.002	0.016	0.005	0.002	0.031	0.028	0.005	0.004	0.003	0.003	0.007	0.005	0.054	0.004	0.01	0.767	0.008	0.014	0.025	0.003
PTWD	P67	0	0.002	0.001	0.001	0.001	0.003	0.003	0.001	0.001	0.002	0.009	0.001	0.001	0.001	0.001	0.001	0.005	0.957	0.003	0.002	0.002	0.002
AMWS	2168	0	0.004	0.001	0.09	0.007	0.002	0.005	0.002	0.204	0.002	0.001	0.002	0.001	0.626	0.001	0.002	0.004	0.002	0.005	0.002	0.036	0.003
AMWS	2279	−4	0.005	0.016	0.001	0.025	0.003	0.01	0.039	0.009	0.012	0.004	0.002	0.013	0.706	0.069	0.005	0.042	0.005	0.014	0.009	0.002	0.011
AMWS	2327	−36	0.002	0.001	0.001	0.001	0.001	0.001	0.003	0.003	0.001	0.001	0.001	0.001	0.975	0.001	0.003	0.001	0.001	0.001	0.001	0.001	0.001
AMWS	987	−1	0.001	0.002	0.001	0.001	0.002	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.974	0.001	0.001	0.001	0.001	0.003	0.003	0.003	0.001
AMWS	988	0	0.004	0.001	0.019	0.002	0.004	0.003	0.002	0.007	0.006	0.007	0.002	0.002	0.897	0.001	0.003	0.025	0.007	0.002	0.004	0.002	0.001
WSSP	1955	−14	0.001	0.001	0.001	0.001	0.004	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.002	0.001	0.001	0.001	0.002	0.977	0.001
WSSP	2139	−1	0.002	0.002	0.001	0.001	0.001	0.002	0.01	0.017	0.002	0.001	0.001	0.001	0.001	0.001	0.001	0.003	0.001	0.001	0.001	0.948	0.001
WSSP	2143	0	0.001	0.001	0.001	0.002	0.001	0.002	0.001	0.001	0.002	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.977	0.002
WSSP	2195	−27	0.003	0.002	0.003	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.004	0.002	0.004	0.002	0.002	0.001	0.003	0.002	0.001	0.962	0.001
WSSP	2286	−5	0.002	0.02	0.001	0.005	0.002	0.001	0.004	0.002	0.001	0.002	0.002	0.001	0.002	0.002	0.002	0.002	0.003	0.002	0.001	0.943	0.001

TABLE 17C

			Populations*																				
Canid Population[a]	Canid ID No.	Missing Data	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42
TURV	1622	−1	0.001	0.002	0.001	0.002	0.004	0.003	0.002	0.001	0.003	0.002	0.001	0.002	0.001	0.002	0.002	0.002	0.001	0.002	0.002	0.958	0.004
TURV	2194	−1	0.003	0.001	0.001	0.008	0.001	0.002	0.005	0.001	0.005	0.002	0.001	0.005	0.002	0.009	0.005	0.016	0.002	0.01	0.004	0.881	0.019
TURV	2200	0	0.003	0.001	0.001	0.002	0.001	0.001	0.001	0.001	0.004	0.005	0.005	0.002	0.002	0.003	0.001	0.008	0.001	0.003	0.001	0.951	0.002
TURV	2222	0	0.003	0.003	0.008	0.004	0.009	0.006	0.006	0.001	0.003	0.004	0.003	0.002	0.002	0.005	0.013	0.001	0.001	0.005	0.007	0.907	0.004
BELS	1351	−1	0.001	0.001	0.001	0.003	0.001	0.001	0.001	0.003	0.002	0.005	0.001	0.001	0.001	0.001	0.001	0.001	0.002	0.001	0.001	0.967	0.002
BELS	2111	−6	0.001	0.004	0.006	0.001	0.001	0.001	0.001	0.001	0.001	0.003	0.002	0.001	0.002	0.002	0.002	0.001	0.008	0.002	0.001	0.954	0.002
BELS	2153	0	0.001	0.001	0.001	0.001	0.001	0	0.001	0.001	0.001	0.003	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.981	0.001
BELS	2209	−1	0.001	0.001	0.001	0.001	0.001	0.001	0.011	0.001	0.001	0.001	0.002	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0	0.973	0.001
BELS	2210	0	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.002	0.001	0.001	0.001	0.001	0.001	0.001	0.004	0.001	0.001	0.976	0.001
OES	1984	−1	0.905	0.004	0.006	0.002	0.006	0.002	0.004	0.002	0.004	0.001	0.001	0.004	0.003	0.006	0.002	0.001	0.003	0.021	0.001	0.002	0.009
OES	2171	−4	0.85	0.004	0.002	0.004	0.003	0.001	0.001	0.002	0.003	0.002	0.003	0.019	0.001	0.018	0.019	0.002	0.004	0.023	0.002	0.001	0.018
OES	2179	−9	0.881	0.025	0.004	0.002	0.002	0.001	0.001	0.007	0.001	0.007	0.012	0.008	0.006	0.004	0.01	0.005	0.006	0.004	0.002	0.005	0.004
OES	1914	−5	0.966	0.001	0.001	0.004	0.002	0.001	0.003	0.001	0.002	0.003	0.001	0.001	0.001	0.002	0.001	0.001	0.002	0.002	0.001	0.001	0.002
OES	2626	−38	0.965	0.001	0.001	0.001	0.003	0.002	0.002	0.001	0.001	0.002	0.002	0.002	0.001	0.002	0.002	0.002	0.001	0.002	0.002	0.002	0.002
BORD	1648	−26	0.003	0.001	0.003	0.003	0.001	0.001	0.001	0.001	0.002	0.004	0.003	0.002	0.002	0.002	0.958	0.003	0.001	0.002	0.001	0.001	0.002
BORD	1828	−17	0.002	0.005	0.023	0.002	0.001	0.01	0.003	0.001	0.001	0.001	0.003	0.002	0.001	0.003	0.749	0.006	0.168	0.003	0.006	0.001	0.004
BORD	1829	−1	0.009	0.003	0.012	0.012	0.021	0.002	0.004	0.003	0.005	0.017	0.001	0.002	0.008	0.018	0.823	0.001	0.002	0.02	0.002	0.005	0.014
BORD	2002	−3	0.006	0.002	0.002	0.003	0.001	0.001	0.001	0.001	0.002	0.005	0.002	0.002	0.001	0.002	0.955	0.002	0.001	0.003	0.001	0.001	0.003
BORD	2003	−3	0.008	0.021	0.002	0.004	0.002	0.004	0.002	0.008	0.002	0.001	0.003	0.005	0.007	0.006	0.886	0.002	0.005	0.005	0.003	0.008	0.011
AUSS	1336	−2	0.011	0.003	0.002	0.009	0.039	0.008	0.003	0.002	0.004	0.01	0.015	0.002	0.003	0.26	0.034	0.002	0.005	0.347	0.016	0.005	0.064
AUSS	1337	−2	0.005	0.006	0.001	0.005	0.013	0.004	0.001	0.001	0.096	0.003	0.002	0.032	0.003	0.015	0.022	0.001	0.002	0.342	0.002	0.003	0.2
AUSS	1500	−15	0.002	0.001	0.003	0.003	0.015	0.002	0.002	0.003	0.004	0.009	0.001	0.001	0.001	0.003	0.005	0.001	0.001	0.003	0.003	0.001	0.472
AUSS	1521	−3	0.128	0.003	0.002	0.08	0.074	0.001	0.002	0.001	0.007	0.002	0.001	0.003	0.002	0.073	0.004	0.003	0.002	0.382	0.002	0.001	0.085
AUSS	1683	−4	0.031	0.004	0.002	0.013	0.005	0.001	0.002	0.001	0.003	0.006	0.002	0.014	0.001	0.128	0.078	0.002	0.002	0.060	0.003	0.002	0.344
COLL	1692	−2	0.001	0.001	0.001	0.002	0.973	0.001	0.001	0.001	0.001	0.001	0.001	0.004	0.002	0.001	0.003	0.001	0.002	0.001	0.002	0.001	0.001
COLL	1701	−11	0.001	0.001	0.001	0.002	0.958	0	0.003	0.002	0.001	0.001	0.003	0.002	0.002	0.003	0.002	0.001	0.001	0.004	0.005	0.002	0.003
COLL	2284	−16	0.001	0.001	0.001	0.001	0.978	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.002	0.001	0.001	0.002
COLL	373	−2	0.001	0	0.001	0.001	0.983	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0	0.001	0.001
COLL	379	−3	0.001	0.001	0.001	0.001	0.978	0	0.001	0.001	0.002	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.002	0.001
SSHP	1379	0	0.005	0.002	0.002	0.01	0.878	0.003	0.006	0.002	0.002	0.012	0.001	0.018	0.003	0.006	0.005	0.002	0.013	0.004	0.001	0.001	0.012
SSHP	1523	−1	0.001	0.008	0.002	0.002	0.868	0.035	0.001	0.003	0.001	0.003	0.008	0.002	0.004	0.006	0.001	0.029	0.005	0.004	0.003	0.003	0.006
SSHP	1824	−6	0.004	0.001	0.006	0.003	0.869	0.001	0.001	0.001	0.001	0.004	0.001	0.011	0.001	0.002	0.004	0.005	0.004	0.003	0.008	0.066	0.003
SSHP	1921	−30	0.002	0.002	0.004	0.001	0.971	0.001	0.001	0.001	0.002	0.002	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.002	0.001	0.001	0.002
SSHP	2040	−19	0.004	0.002	0.001	0.001	0.907	0.002	0.006	0.003	0.002	0.004	0.001	0.003	0.001	0.013	0.004	0.002	0.002	0.009	0.001	0.018	0.007
DACH	1051	−5	0.002	0.001	0.001	0.002	0.001	0.001	0.001	0.003	0.002	0.001	0.002	0.002	0.002	0.002	0.002	0.001	0.001	0.002	0.968	0.001	0.001
DACH	1052	−2	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.984	0.001	0.001
DACH	1053	−2	0.012	0.005	0.002	0.002	0.002	0.002	0.002	0.016	0.001	0.002	0.001	0.002	0.004	0.005	0.002	0.007	0.004	0.003	0.915	0.002	0.005
DACH	1054	0	0.001	0.001	0.001	0.002	0.001	0.014	0.001	0.002	0.001	0.002	0.001	0.001	0.001	0.002	0.001	0.001	0.001	0.001	0.961	0.001	0.001
DACH	1055	−1	0.001	0.001	0.002	0.001	0.002	0.001	0.002	0.001	0.001	0.002	0.003	0.001	0.001	0.002	0.001	0.001	0.001	0.002	0.971	0.002	0.001
DANE	1574	−5	0.004	0.922	0.002	0.002	0.003	0.002	0.001	0.002	0.001	0.001	0.003	0.002	0.001	0.002	0.001	0.005	0.037	0.001	0.002	0.004	0.001
DANE	1575	−11	0.004	0.9	0.002	0.002	0.001	0.032	0.001	0.001	0.002	0.001	0.002	0.002	0.003	0.006	0.002	0.001	0.02	0.005	0.006	0.002	0.003
DANE	1580	−2	0.002	0.977	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.002	0.001	0.001	0.001	0.001	0.001	0.001	0.002	0.001
DANE	1700	−7	0.002	0.934	0.003	0.002	0.004	0.001	0.002	0.004	0.002	0.012	0.001	0.001	0.002	0.002	0.002	0.013	0.001	0.002	0.001	0.006	0.002
DANE	1748	−3	0.001	0.973	0.001	0.001	0.001	0.001	0.002	0.001	0.001	0.001	0.004	0.001	0.001	0.001	0.002	0.001	0.001	0.001	0.001	0.001	0.001
IWOF	1581	−21	0.001	0.001	0.001	0.001	0	0	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.985	0.001	0.001	0	0.001	0.001
IWOF	1761	−12	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.981	0.001	0.001	0.001	0.001	0.001
IWOF	1792	−4	0.001	0.001	0.003	0.002	0.001	0.001	0.001	0.001	0.001	0.002	0.001	0.001	0.001	0.001	0.001	0.972	0.003	0.001	0.002	0.001	0.001

TABLE 17C-continued

			Populations*																				
Canid Population[a]	Canid ID No.	Missing Data	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42
IWOF	1906	−6	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.982	0.002	0.001	0.001	0.001	0.001
IWOF	1993	−3	0.002	0.001	0.001	0.001	0.001	0.001	0.001	0.003	0.001	0.002	0.001	0.001	0.001	0.001	0	0.972	0.001	0.001	0.001	0.006	0.001
BORZ	1378	0	0.004	0.001	0.001	0.002	0.004	0.001	0.944	0.007	0.001	0.003	0.002	0.007	0.003	0.003	0.002	0.001	0.001	0.004	0.002	0.001	0.003
BORZ	1401	−4	0.001	0.001	0.002	0.001	0.001	0.001	0.979	0.001	0	0.001	0.001	0.001	0.002	0.001	0.001	0.003	0.001	0.001	0.001	0	0.001
BORZ	1808	−2	0.001	0.004	0.001	0.003	0.001	0.002	0.959	0.001	0.001	0.001	0.004	0.001	0.002	0.002	0.001	0.001	0.003	0.003	0.002	0.001	0.003
BORZ	2268	0	0.003	0.003	0.002	0.002	0.008	0.004	0.858	0.004	0.002	0.012	0.005	0.002	0.002	0.007	0.002	0.058	0.002	0.005	0.004	0.004	0.006
BORZ	978	−1	0.003	0.008	0.001	0.004	0.002	0.001	0.936	0.001	0.011	0.006	0.006	0.003	0.003	0.002	0.001	0.001	0.001	0.002	0.001	0.005	0.001
GREY	2477	−1	0.002	0.001	0.001	0.001	0.001	0.001	0.019	0.023	0.001	0.864	0.008	0.002	0.001	0.012	0.001	0.018	0.005	0.011	0.001	0.003	0.015
GREY	2478	0	0.001	0.004	0.01	0.002	0.002	0.002	0.001	0.002	0.006	0.951	0.001	0.001	0.003	0.002	0.001	0.001	0.001	0.002	0.002	0.001	0.002
GREY	2479	0	0.004	0.002	0.001	0.007	0.003	0.001	0.005	0.001	0.004	0.932	0.009	0.002	0.003	0.004	0.002	0.004	0.002	0.005	0.001	0.001	0.004
GREY	2480	−3	0.002	0.001	0.001	0.004	0.004	0.011	0.004	0.001	0.001	0.929	0.002	0.001	0.002	0.006	0.001	0.012	0.002	0.005	0.001	0.003	0.003
GREY	2481	−3	0.001	0.004	0.002	0.013	0.002	0.004	0.012	0.045	0.006	0.829	0.004	0.001	0.002	0.011	0.005	0.017	0.001	0.006	0.002	0.003	0.012
WHIP	1355	−1	0.003	0.001	0.002	0.001	0.001	0.001	0.002	0.001	0.002	0.96	0.004	0.008	0.002	0.002	0.001	0.002	0.001	0.002	0.001	0.001	0.001
WHIP	1395	−42	0.003	0.002	0.004	0.006	0.001	0.004	0.022	0.005	0.003	0.61	0.001	0.002	0.002	0.006	0.02	0.148	0.004	0.02	0.004	0.002	0.067
WHIP	1407	−2	0.001	0.001	0.001	0.002	0.001	0.002	0.002	0.002	0.002	0.881	0.002	0.005	0.002	0.003	0.002	0.083	0.001	0.002	0.002	0.002	0.002
WHIP	1409	−2	0.001	0.001	0.001	0.001	0.002	0.001	0.001	0.002	0.001	0.97	0.001	0.002	0.001	0.001	0.001	0.007	0.001	0.001	0.001	0.002	0.001
WHIP	1518	−14	0.001	0.001	0.001	0.003	0.003	0.001	0.001	0.002	0.001	0.942	0.006	0.012	0.001	0.003	0.002	0.001	0.001	0.003	0.001	0.001	0.006
ITGR	1568	−1	0.001	0.004	0.008	0.002	0.001	0.004	0.001	0.001	0.008	0.002	0.95	0.001	0.002	0.002	0.001	0.003	0.001	0.002	0.001	0.003	0.001
ITGR	1570	−25	0.001	0.001	0.001	0.001	0.001	0.004	0.002	0.001	0.001	0.001	0.975	0.002	0.001	0.001	0.001	0.002	0.001	0.001	0.001	0.001	0.001
ITGR	1862	−5	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0	0.001	0.001	0.978	0.002	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001
ITGR	1881	−12	0.001	0.001	0.001	0.002	0.001	0.001	0.001	0.001	0.006	0.002	0.949	0.004	0.001	0.003	0.003	0.001	0.005	0.002	0.004	0.003	0.003
ITGR	1882	−3	0.001	0.002	0.001	0.001	0.001	0.001	0.004	0.002	0.001	0.002	0.972	0.002	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001
RHOD	1444	−16	0.002	0.001	0.006	0.003	0.043	0.002	0.001	0.001	0.002	0.001	0.002	0.004	0.002	0.002	0.004	0.001	0.908	0.003	0.002	0.002	0.003
RHOD	1454	−2	0.035	0.003	0.01	0.014	0.004	0.001	0.002	0.002	0.002	0.015	0.014	0.004	0.01	0.011	0.002	0.009	0.695	0.008	0.003	0.002	0.071
RHOD	1505	−3	0.03	0.023	0.003	0.036	0.002	0.014	0.002	0.001	0.03	0.003	0.002	0.008	0.005	0.01	0.003	0.009	0.774	0.023	0.002	0.002	0.009
RHOD	1592	−14	0.001	0.001	0.002	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.002	0.001	0.001	0.001	0.001	0.001	0.979	0.001	0.002	0.001	0.001
RHOD	1609	−50	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.003	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.977	0.001	0.001	0.001	0.001
STBD	1075	−1	0.006	0.005	0.005	0.026	0.003	0.005	0.002	0.838	0.017	0.005	0.001	0.002	0.012	0.02	0.004	0.002	0.001	0.011	0.001	0.017	0.01
STBD	1714	−5	0.001	0.001	0.001	0.002	0.001	0.001	0.001	0.98	0.001	0.001	0	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001
STBD	1750	−22	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.982	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0	0.001
STBD	2403	−17	0.001	0.002	0.001	0.001	0.003	0.001	0.005	0.967	0.001	0.001	0.001	0.005	0.001	0.001	0.001	0.001	0.001	0.001	0.002	0.002	0.001
STBD	2404	−2	0.001	0.001	0.002	0.001	0.002	0	0.001	0.975	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.003	0.002	0.001	0.002	0.001	0.001
CLSP	1008	−1	0.001	0.003	0.003	0.001	0.001	0.976	0	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.003	0.001	0.001	0.001	0.001	0.001
CLSP	1009	0	0	0.001	0	0.001	0.001	0.988	0	0.001	0.001	0.001	0.001	0	0	0.001	0.001	0.001	0	0.001	0.001	0	0.001
CLSP	1802	−2	0	0.001	0	0	0	0.992	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CLSP	2312	−1	0.001	0.001	0.001	0.002	0.001	0.978	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001

TABLE 17C-continued

			Populations*																				
Canid Population[a]	Canid ID No.	Missing Data	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42
CLSP	2314	0	0	0	0.001	0.001	0.001	0.988	0	0.001	0	0.001	0.001	0	0	0.001	0.001	0	0.001	0.001	0	0	0.001
AUST	1387	−3	0.006	0.006	0.002	0.003	0.006	0.001	0.003	0.001	0.002	0.004	0.011	0.91	0.004	0.003	0.002	0.015	0.002	0.005	0.003	0.002	0.005
AUST	1531	−1	0.003	0.004	0.002	0.002	0.004	0.007	0.005	0.002	0.018	0.002	0.001	0.899	0.004	0.005	0.017	0.003	0.002	0.005	0.005	0.002	0.004
AUST	1564	−7	0.001	0.001	0.001	0.002	0.003	0	0.001	0.001	0.001	0.001	0.003	0.973	0.002	0.001	0.002	0.001	0.001	0.002	0.001	0.001	0.002
AUST	1870	−5	0.001	0.001	0.002	0.002	0.003	0.003	0.011	0.001	0.001	0.001	0.001	0.95	0.001	0.003	0.002	0.001	0.001	0.004	0.003	0.001	0.003
AUST	1871	0	0.012	0.009	0.005	0.016	0.002	0.002	0.002	0.003	0.002	0.014	0.001	0.806	0.007	0.006	0.004	0.002	0.083	0.007	0.001	0.003	0.007
WHWT	1388	−13	0.002	0.001	0.001	0.001	0.002	0.007	0.004	0.001	0.954	0.002	0.007	0.002	0.002	0.002	0.001	0.001	0.001	0.002	0.002	0.002	0.002
WHWT	1420	−7	0.001	0.001	0.001	0.003	0.001	0.001	0.001	0.113	0.856	0.003	0.001	0.002	0.001	0.002	0.002	0.001	0.001	0.002	0.001	0.001	0.002
WHWT	1992	−5	0.002	0.001	0.001	0.003	0.001	0.006	0.001	0.001	0.968	0.001	0.001	0.001	0.001	0.001	0.001	0.003	0.001	0.001	0.001	0.002	0.001
WHWT	2100	−4	0.002	0.003	0.005	0.003	0.006	0.001	0.001	0.003	0.948	0.002	0.002	0.001	0.001	0.003	0.002	0.001	0.001	0.003	0.005	0.003	0.002
WHWT	2128	0	0.002	0.001	0.001	0.002	0.001	0	0.001	0.001	0.979	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001
CAIR	1405	−1	0.002	0.002	0.002	0.638	0.002	0.007	0.001	0.004	0.28	0.006	0.001	0.002	0.011	0.008	0.004	0.003	0.002	0.008	0.002	0.004	0.004
CAIR	2096	−28	0.001	0.001	0.003	0.857	0.002	0.002	0.002	0.001	0.076	0.005	0.011	0.002	0.003	0.004	0.001	0.001	0.002	0.005	0.003	0.001	0.007
CAIR	2113	−4	0.003	0.003	0.003	0.693	0.001	0.001	0.004	0.001	0.242	0.004	0.004	0.002	0.004	0.005	0.002	0.001	0.002	0.006	0.003	0.003	0.006
CAIR	2125	−1	0.005	0.001	0.005	0.619	0.001	0.001	0.001	0.001	0.332	0.004	0.002	0.002	0.002	0.004	0.001	0.001	0.004	0.003	0.001	0.005	0.003
CAIR	2131	−8	0.009	0.003	0.002	0.917	0.005	0.003	0.003	0.002	0.007	0.005	0.002	0.004	0.003	0.004	0.01	0.001	0.001	0.005	0.001	0.002	0.006
BEDT	1422	−5	0.001	0	0.987	0.001	0.001	0.001	0	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0	0.001
BEDT	1423	−8	0	0.001	0.986	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0	0.001	0.001	0.001	0.001	0	0.001
BEDT	1424	−21	0.001	0.001	0.982	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001
BEDT	1426	−30	0.001	0.001	0.981	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001
CHIH	1202	−8	0.002	0.002	0.002	0.002	0.003	0.001	0.001	0.003	0.001	0.001	0.002	0.002	0.963	0.002	0.001	0.002	0.003	0.002	0.002	0.002	0.001
CHIH	1203	−4	0.001	0.001	0.001	0.003	0.001	0.001	0.001	0.001	0.002	0.001	0.001	0.002	0.969	0.002	0.001	0.001	0.001	0.002	0.002	0.002	0.001
CHIH	1204	0	0.003	0.002	0.002	0.005	0.001	0.002	0.009	0.002	0.002	0.013	0.001	0.006	0.921	0.006	0.003	0.002	0.001	0.007	0.001	0.001	0.005
CHIH	1205	−2	0.013	0.003	0.001	0.007	0.003	0.004	0.001	0.001	0.002	0.002	0.001	0.001	0.417	0.176	0.003	0.001	0.005	0.113	0.004	0.005	0.118
CHIH	1206	−1	0.001	0.001	0.003	0.409	0.002	0.007	0.001	0.003	0.002	0.018	0.005	0.029	0.405	0.013	0.018	0.012	0.006	0.011	0.005	0.007	0.021

TABLE 17D

			Populations*																				
Canid Population^a	Canid ID No.	Missing Data	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85
CHBR	1546	−4	0.002	0.832	0.008	0.001	0.006	0.003	0.002	0.004	0.004	0.006	0.031	0.008	0.003	0.007	0.044	0.005	0.014	0.009	0.002	0.002	0.006
CHBR	1549	−4	0.001	0.955	0.001	0.002	0.001	0.001	0.004	0.003	0.004	0.003	0.002	0.004	0.001	0.002	0.003	0.001	0.002	0.004	0.001	0.003	0.001
CHBR	1813	−3	0.001	0.951	0.002	0.001	0.003	0.003	0.002	0.003	0.002	0.002	0.002	0.002	0.005	0.003	0.006	0.002	0.002	0.001	0.003	0.003	0.001
CHBR	2091	−1	0.003	0.868	0.005	0.001	0.003	0.003	0.001	0.004	0.022	0.021	0.002	0.007	0.002	0.002	0.007	0.007	0.004	0.027	0.001	0.002	0.009
CHBR	888	−12	0.002	0.959	0.001	0.009	0.001	0.001	0.001	0.001	0.002	0.001	0.001	0.001	0.001	0.001	0.001	0.002	0.002	0.001	0.002	0.001	0.01
FCR	1188	−1	0.002	0.001	0.001	0.001	0.221	0.001	0.001	0.001	0.001	0.001	0.005	0.002	0.002	0.001	0.001	0.002	0.002	0.748	0.001	0.001	0.004
FCR	2020	−11	0.001	0.005	0.001	0.001	0.215	0.001	0.001	0.001	0.002	0.001	0.002	0.001	0.001	0.001	0.003	0.001	0.002	0.759	0.001	0.001	0.001
FCR	2042	−7	0.002	0.001	0.001	0.001	0.221	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0	0.001	0.001	0.001	0.759	0.001	0.004	0.001
FCR	2044	0	0.002	0.009	0.001	0.001	0.193	0.002	0.007	0.001	0.001	0.001	0.003	0.004	0.004	0.002	0.002	0.001	0.002	0.746	0.001	0.011	0.004
FCR	2259	0	0.005	0.001	0.001	0.001	0.213	0.008	0.002	0.002	0.001	0.001	0.001	0.001	0.001	0.001	0.002	0.001	0.001	0.754	0.001	0.001	0.002
GOLD	591	−3	0.003	0.002	0.003	0.002	0.001	0.002	0.004	0.004	0.001	0.005	0.027	0.003	0.001	0.001	0.925	0.002	0.003	0.01	0.001	0.001	0.001
GOLD	592	−3	0.001	0.009	0.001	0.003	0.01	0.001	0.002	0.005	0.004	0.01	0.144	0.07	0.003	0.001	0.642	0.005	0.019	0.063	0.001	0.002	0.003
GOLD	593	−1	0.002	0.003	0.001	0.001	0.001	0.007	0.003	0.001	0.002	0.003	0.006	0.003	0.004	0.001	0.95	0.002	0.003	0.002	0.002	0.001	0.003
GOLD	603	0	0.001	0.002	0.001	0.002	0.001	0.001	0.001	0.002	0.001	0.001	0.001	0.001	0.002	0.001	0.979	0.001	0.001	0.001	0.001	0.001	0
GOLD	604	0	0.001	0.002	0.001	0.001	0.009	0.002	0.002	0.004	0.002	0.001	0.001	0.002	0.004	0.011	0.939	0.003	0.002	0.005	0.002	0.001	0.003
LAB	1310	−2	0.008	0.002	0.005	0.102	0.003	0.016	0.002	0.019	0.01	0.012	0.547	0.045	0.001	0.008	0.002	0.004	0.029	0.179	0.003	0.003	0.002
LAB	1465	−2	0.001	0.003	0.001	0.001	0.002	0.001	0.001	0.001	0.001	0.001	0.745	0.001	0.003	0.002	0.002	0.001	0.001	0.23	0.001	0.001	0.001
LAB	1468	−12	0.001	0.004	0.001	0.001	0.005	0.005	0.005	0.001	0.004	0.002	0.728	0.004	0.002	0.001	0.001	0.001	0.002	0.222	0.001	0.005	0.001
LAB	1754	−12	0.023	0.002	0.002	0.001	0.001	0.002	0.001	0.009	0.005	0.004	0.703	0.004	0.002	0.003	0.006	0.002	0.007	0.214	0.006	0.001	0.001
LAB	1830	−17	0.001	0.003	0.005	0.021	0.001	0.009	0.003	0.013	0.003	0.002	0.359	0.082	0.001	0.006	0.027	0.001	0.363	0.095	0.002	0.001	0.002
GSD	1666	−23	0.002	0.001	0.001	0	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.006	0.977	0.001	0.001	0.001	0.001	0.001	0.001	0.001
GSD	1776	−9	0.001	0.001	0.001	0.001	0.001	0.001	0.002	0.001	0.001	0.001	0.001	0.001	0.003	0.98	0.001	0.001	0.001	0.001	0.001	0.002	0.001
GSD	2011	−2	0.001	0.001	0.001	0.003	0.001	0.002	0.001	0.001	0.001	0.001	0.001	0.001	0.002	0.975	0.001	0.001	0.002	0.001	0.001	0.001	0.001
GSD	2060	−2	0.001	0.001	0.001	0.001	0.003	0.001	0.002	0.001	0.001	0.002	0.001	0.001	0.001	0.977	0.001	0.001	0.001	0.001	0.001	0.001	0.001
GSD	2086	−6	0.003	0.003	0.005	0.001	0.001	0.002	0.001	0.002	0.002	0.001	0.003	0.002	0.003	0.961	0.002	0.001	0.003	0.002	0.001	0.001	0.002
IRTR	2152	−4	0.75	0.055	0.008	0.053	0.007	0.001	0.001	0.013	0.004	0.003	0.008	0.034	0.002	0.002	0.005	0.003	0.009	0.036	0.001	0.002	0.002
IRTR	2189	−4	0.987	0.001	0.001	0.001	0.001	0	0	0	0.001	0.001	0.001	0.001	0.001	0	0	0.001	0	0.001	0.001	0	0.001
IRTR	2238	−1	0.973	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.002	0.001	0.001	0.001	0.001	0.003	0.001	0.001	0.004
IRTR	2242	−1	0.984	0.001	0.001	0.001	0.001	0	0.001	0.002	0.001	0.001	0.001	0.001	0.001	0	0.001	0.001	0.001	0.001	0.001	0.001	0.001
KERY	13878	0	0.007	0.042	0.006	0.003	0.001	0.001	0.002	0.002	0.91	0.002	0.003	0.003	0.005	0.001	0.001	0.001	0.001	0.002	0.003	0.001	0.001
KERY	1483	−11	0.001	0.002	0.001	0.002	0.001	0.001	0.001	0.001	0.975	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.002	0.002	0.001	0.003
KERY	1579	−2	0.002	0.001	0.001	0.004	0.001	0.001	0.001	0.002	0.968	0.001	0.003	0.001	0.001	0.001	0.004	0.001	0.002	0.002	0.001	0.001	0.001
KERY	2014	0	0.003	0.058	0.003	0.002	0.001	0.004	0.001	0.009	0.852	0.006	0.006	0.005	0.002	0.002	0.002	0.028	0.004	0.002	0.002	0.001	0.007
KERY	24255	−1	0.001	0.001	0.001	0.134	0.002	0.001	0.001	0.001	0.826	0.001	0.001	0.001	0.001	0.001	0.001	0.003	0.002	0.001	0.002	0.013	0.005
SCWT	1624	−30	0.001	0.001	0.001	0.978	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.002	0.003	0.001
SCWT	1770	−4	0.004	0.001	0.001	0.973	0.001	0.001	0.001	0.001	0.005	0.001	0.001	0.001	0.001	0	0.001	0.001	0.002	0.001	0.004	0.001	0.001
SCWT	2250	−6	0.003	0.001	0.001	0.982	0.001	0.001	0	0.001	0.001	0.001	0.001	0.001	0.001	0.002	0.001	0.001	0.001	0.001	0.001	0.001	0.001
SCWT	2301	−15	0.001	0.002	0.001	0.975	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.002	0.001	0	0.001	0.003	0.001	0.001	0.002
POM	1190	−2	0.001	0.002	0.001	0.003	0.004	0.001	0.004	0.002	0.004	0.002	0.004	0.005	0.026	0.001	0.008	0.895	0.022	0.003	0.003	0.003	0.006
POM	1191	−2	0.001	0.002	0.003	0.005	0.005	0.009	0.004	0.02	0.004	0.002	0.005	0.004	0.003	0.009	0.002	0.892	0.003	0.007	0.011	0.008	0.002
POM	1210	−8	0.007	0.003	0.003	0.007	0.004	0.007	0.007	0.001	0.003	0.007	0.004	0.007	0.007	0.002	0.003	0.908	0.003	0.002	0.001	0.008	0.005
POM	1238	0	0.003	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.002	0.002	0.001	0.002	0.001	0.001	0.001	0.975	0.001	0.001	0.001	0.001	0.001
POM	1239	−14	0.004	0.005	0.002	0.003	0.001	0.001	0.001	0.002	0.003	0.002	0.03	0.352	0.002	0.001	0.005	0.553	0.025	0.001	0.002	0.002	0.002
SCHP	1386	−9	0.008	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.002	0.002	0.001	0.001	0.001	0.001	0.002	0.001	0.001	0.002	0.001	0.001	0.969
SCHP	1471	−13	0.002	0.001	0.001	0.001	0.002	0.002	0.001	0.001	0.001	0.002	0.001	0.001	0.001	0.002	0.001	0.001	0.001	0.003	0.001	0.001	0.972
SCHP	1814	−1	0.001	0.001	0.001	0.001	0.001	0.002	0.028	0.002	0.001	0.001	0.001	0.002	0.006	0.002	0.004	0.002	0.001	0.001	0.001	0.001	0.941
SCHP	1852	0	0.001	0.001	0.001	0.004	0.001	0.001	0.001	0.001	0.001	0.003	0.002	0.001	0.002	0.001	0.001	0.002	0.001	0.004	0.001	0.002	0.966

TABLE 17D-continued

			Populations*																				
Canid Population[a]	Canid ID No.	Missing Data	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85
BMD	941	−11	0.001	0.003	0.001	0.002	0.004	0.014	0.007	0.002	0.002	0.002	0.001	0.002	0.94	0.001	0.003	0.003	0.004	0.001	0.001	0.005	0.001
BMD	943	−10	0.002	0.002	0.001	0.002	0.002	0.005	0.002	0.001	0.002	0.002	0.005	0.005	0.869	0.002	0.002	0.087	0.004	0.002	0.001	0.002	0.001
BMD	968	−15	0.001	0.001	0.001	0.001	0.001	0.002	0.002	0.002	0.001	0.001	0.001	0.002	0.973	0.001	0.004	0.001	0.001	0.001	0.001	0.001	0.001
BMD	1763	−10	0.012	0.003	0.002	0.002	0.005	0.003	0.003	0.002	0.012	0.002	0.001	0.002	0.916	0.005	0.007	0.005	0.002	0.002	0.01	0.001	0.003
BMD	969	−2	0.001	0.001	0.001	0.001	0.013	0.002	0.001	0.003	0.004	0.001	0.002	0.001	0.954	0.002	0.002	0.001	0.002	0.002	0.002	0.003	0.001
GSMD	1547	−4	0.001	0.001	0.001	0.001	0	0.001	0.001	0	0.001	0.001	0.001	0.001	0.986	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001
GSMD	1659	0	0.002	0.001	0.001	0.001	0.001	0.001	0.003	0.001	0.002	0.001	0.001	0.001	0.976	0.001	0.002	0.002	0.001	0.001	0.001	0.001	0.001
GSMD	1660	−4	0.003	0.003	0.007	0.005	0.001	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.932	0.023	0.001	0.002	0.002	0.001	0.001	0.001	0.001
GSMD	1662	−42	0.001	0.004	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.002	0.97	0.001	0.002	0.001	0.004	0.001	0.002	0.001	0.001
GSMD	1663	−5	0.001	0.001	0	0.001	0	0.001	0	0.001	0.001	0	0.001	0.001	0.988	0.001	0	0.001	0	0.001	0.001	0	0.001
BOX	1176	0	0.001	0.001	0	0	0.981	0.001	0.001	0.001	0.001	0.002	0.001	0.001	0.002	0.001	0.001	0.001	0.001	0.001	0.002	0.001	0.001
BOX	1177	−1	0.004	0.021	0.002	0.002	0.912	0.001	0.006	0.002	0.002	0.003	0.002	0.003	0.002	0.002	0.006	0.014	0.003	0.005	0.002	0.002	0.003
BOX	1178	0	0.001	0.001	0.003	0.001	0.978	0.001	0.001	0.002	0.002	0.001	0.001	0.001	0	0.001	0.001	0.001	0.001	0.001	0.002	0.001	0.001
BOX	1179	−3	0.001	0	0.001	0	0.988	0.001	0.001	0.001	0	0.001	0.001	0.001	0.001	0	0	0.001	0.001	0	0.001	0.001	0.001
BOX	1304	−1	0.001	0.001	0.001	0.001	0.984	0.001	0.001	0.001	0.001	0.002	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001
MBLT	1915	−5	0.003	0.001	0.956	0.001	0.002	0.001	0.001	0.002	0.003	0.002	0.002	0.002	0.001	0.001	0.001	0.001	0.002	0.004	0.002	0.004	0.01
MBLT	2253	−12	0.001	0.001	0.979	0.002	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.002	0.001	0.001	0.001	0.001
MBLT	2254	−33	0.001	0.001	0.989	0.001	0.001	0.001	0.001	0.001	0	0.001	0.001	0.001	0	0	0.001	0.001	0.001	0.001	0.001	0.001	0.001
MBLT	2255	−23	0.002	0.001	0.98	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.004	0.001	0.001	0.001
MBLT	2256	−34	0.001	0.001	0.981	0.001	0.002	0.002	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.002	0.001
BULD	1193	−1	0.001	0.002	0.003	0.001	0.002	0.002	0.001	0.003	0.009	0.003	0.005	0.002	0.002	0.001	0.001	0.002	0.006	0.002	0.001	0.952	0.001
BULD	1194	−2	0.001	0.001	0.001	0.009	0.001	0.002	0.002	0.003	0.002	0.002	0.002	0.002	0.001	0	0.001	0.003	0.001	0.001	0.009	0.952	0.002
BULD	1195	−8	0.005	0.001	0.001	0.002	0.001	0.001	0.001	0.003	0.001	0.002	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.974	0.001
BULD	1197	−3	0.001	0.001	0.002	0.001	0.001	0.001	0.005	0.001	0.001	0.001	0.003	0.002	0.001	0.001	0.001	0.001	0.002	0.002	0.001	0.97	0.001
BULD	1198	0	0.001	0.004	0.002	0.001	0.002	0.002	0.001	0.005	0.003	0.003	0.002	0.002	0.005	0.001	0.001	0.003	0.002	0.002	0.013	0.944	0.001
FBLD	1507	−9	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.984	0.001	0.001
FBLD	1508	−7	0.001	0.003	0.003	0.004	0.004	0.002	0.001	0.003	0.008	0.003	0.002	0.002	0.001	0.001	0.002	0.01	0.002	0.001	0.939	0.002	0.004
FBLD	1509	−5	0.001	0.001	0.002	0.002	0.002	0.001	0.002	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.95	0.029	0.001
FBLD	2671	−15	0.017	0.001	0.05	0.003	0.001	0.001	0.001	0.003	0.001	0.002	0.001	0.002	0.002	0.001	0.002	0.001	0.004	0.001	0.9	0.001	0.004
PRES	1082	−4	0.002	0.003	0.12	0.001	0.012	0.002	0.001	0.016	0.002	0.002	0.043	0.015	0.002	0.001	0.001	0.003	0.757	0.002	0.002	0.013	0.002
PRES	1096	0	0.003	0.018	0.003	0.001	0.007	0.006	0.002	0.007	0.05	0.748	0.002	0.008	0.002	0.032	0.001	0.002	0.014	0.005	0.001	0.082	0.008
PRES	1115	0	0.001	0.002	0.015	0.002	0.016	0.002	0.001	0.003	0.002	0.926	0.002	0.003	0.001	0.001	0.009	0.001	0.003	0.002	0.003	0.003	0.001
PRES	1127	−7	0.002	0.021	0.003	0.001	0.011	0.002	0.006	0.002	0.001	0.817	0.01	0.017	0.004	0.002	0.004	0.006	0.004	0.003	0.02	0.059	0.005
PRES	1095	−5	0.005	0.003	0.009	0.013	0.006	0.002	0.002	0.014	0.007	0.909	0.003	0.004	0.002	0.002	0.002	0.002	0.003	0.001	0.005	0.003	0.002

TABLE 17D-continued

			Populations*																				
Canid Population[a]	Canid ID No.	Missing Data	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85
BULM	1105	0	0.008	0.003	0.003	0.002	0.008	0.011	0.001	0.922	0.001	0.005	0.002	0.003	0.003	0.001	0.005	0.002	0.004	0.002	0.004	0.006	0.002
BULM	1106	−3	0.002	0.009	0.003	0.002	0.001	0.004	0.001	0.902	0.002	0.007	0.007	0.004	0.002	0.001	0.024	0.002	0.006	0.002	0.003	0.006	0.007
BULM	1107	−1	0.002	0.002	0.001	0.001	0.003	0.001	0.001	0.972	0.001	0.001	0.001	0.002	0.001	0.001	0.001	0.002	0.002	0.002	0.001	0.001	0.001
BULM	1108	0	0.016	0.01	0.065	0.005	0.001	0.002	0.001	0.844	0.004	0.015	0.003	0.004	0.002	0.008	0.002	0.003	0.003	0.003	0.002	0.003	0.004
BULM	1109	0	0.005	0.001	0.007	0.004	0.007	0.001	0.002	0.915	0.002	0.01	0.003	0.003	0.001	0.005	0.002	0.003	0.003	0.006	0.001	0.018	0.001
MAST	1015	0	0.001	0.001	0.004	0.002	0.001	0.001	0.001	0.968	0.004	0.001	0.001	0.002	0.002	0.001	0.003	0.002	0.001	0.001	0.002	0.001	0.001
MAST	1016	0	0.002	0.002	0.001	0.001	0.001	0.001	0.001	0.911	0.003	0.002	0.002	0.002	0.003	0.001	0.001	0.002	0.004	0.001	0.002	0.055	0.001
MAST	1017	−25	0.002	0.001	0.001	0.002	0.002	0.002	0.001	0.964	0.002	0.002	0.001	0.002	0.002	0.003	0.002	0.001	0.002	0.002	0.001	0.002	0.003
MAST	1066	−3	0.001	0.002	0.002	0.001	0.001	0.001	0.002	0.962	0.002	0.001	0.002	0.003	0.001	0.001	0.002	0.001	0.007	0.001	0.003	0.003	0.001
MAST	991	−18	0.002	0.001	0.001	0.001	0.001	0.001	0.001	0.977	0.003	0.001	0.001	0.001	0.001	0.002	0.001	0.001	0.001	0.001	0.001	0.001	0.001
NEWF	271	−2	0.002	0.004	0.001	0.001	0.005	0.874	0.01	0.002	0.002	0.016	0.006	0.009	0.006	0.002	0.01	0.015	0.006	0.014	0.005	0.005	0.004
NEWF	274	−1	0.001	0.001	0.002	0.001	0.001	0.968	0.001	0.002	0.001	0.001	0.005	0.002	0.002	0.002	0.002	0.001	0.002	0.002	0.001	0.001	0.001
NEWF	275	−2	0.002	0.002	0.001	0.001	0.001	0.979	0.002	0.001	0.001	0.001	0.001	0.001	0.001	0.003	0.001	0.001	0.001	0.001	0.001	0.001	0
NEWF	277	0	0.002	0.001	0.001	0.001	0.006	0.904	0.005	0.02	0.001	0.002	0.034	0.002	0.001	0.004	0.001	0.001	0.003	0.011	0.001	0.001	0.001
NEWF	278	−2	0.002	0.003	0.001	0.001	0.002	0.667	0.003	0.005	0.002	0.203	0.013	0.057	0.001	0.015	0.003	0.004	0.01	0.004	0.002	0.002	0.001
ROTT	1014	−2	0.003	0.005	0.001	0.004	0.001	0.011	0.933	0.002	0.001	0.001	0.002	0.004	0.008	0.004	0.002	0.004	0.005	0.001	0.004	0.002	0.002
ROTT	1028	−3	0.001	0.001	0	0	0.001	0.003	0.981	0	0	0.001	0.001	0.001	0.001	0.001	0.002	0.001	0.001	0.001	0.001	0.001	0.001
ROTT	1029	−1	0.001	0.002	0.002	0.006	0.001	0.007	0.939	0.001	0.001	0.001	0.004	0.003	0.007	0.008	0.004	0.001	0.002	0.003	0.002	0.002	0.001
ROTT	1033	−4	0.002	0.002	0.003	0.001	0.001	0.003	0.963	0.002	0.001	0.003	0.002	0.003	0.001	0.001	0.002	0.001	0.004	0.001	0.001	0.002	0.002
ROTT	1034	0	0.001	0.002	0.001	0.001	0.004	0.001	0.967	0.001	0.002	0.001	0.001	0.001	0.004	0.003	0.001	0.001	0.001	0.001	0.004	0.001	0.001

[a] See Table 5 for abbreviations of canid populations.

*All values for the populations that are not shown are zero.

KBB: pbe

TABLE 18A-F

Population	Canid ID No.		
AMAL	1629	0.998	0.002
AMAL	1779	0.997	0.003
AMAL	1845	0.997	0.003
AMAL	2132	0.987	0.013
AMAL	2214	0.997	0.003
HUSK	1469	0.003	0.997
HUSK	1883	0.001	0.999
HUSK	2115	0.003	0.997
HUSK	2117	0.006	0.994
HUSK	2118	0.005	0.995
BULM	1105	0.003	0.997
BULM	1106	0.002	0.998
BULM	1107	0.002	0.998
BULM	1108	0.006	0.994
BULM	1109	0.003	0.997
MAST	1015	0.998	0.002
MAST	1016	0.997	0.003
MAST	1017	0.995	0.005
MAST	1066	0.997	0.003
MAST	991	0.995	0.005
BMD	941	0.002	0.998
BMD	943	0.003	0.997
BMD	968	0.001	0.999
BMD	1763	0.002	0.998
BMD	969	0.002	0.998
GSMD	1547	0.998	0.002
GSMD	1659	0.997	0.003
GSMD	1660	0.999	0.001
GSMD	1662	0.997	0.003
GSMD	1663	0.998	0.002
GREY	2477	0.005	0.995
GREY	2478	0.007	0.993
GREY	2479	0.003	0.997
GREY	2480	0.003	0.997
GREY	2481	0.005	0.995
WHIP	1355	0.993	0.007
WHIP	1395	0.992	0.008
WHIP	1407	0.919	0.081
WHIP	1409	0.997	0.003
WHIP	1518	0.976	0.024
BELS	1351	0.515	0.485
BELS	2111	0.515	0.485
BELS	22153	0.504	0.496
BELS	2209	0.504	0.496
BELS	2210	0.522	0.478
TURV	1622	0.517	0.483
TURV	2194	0.521	0.479
TURV	2200	0.527	0.473
TURV	2222	0.514	0.486
COLL	1692	0.003	0.997
COLL	1701	0.005	0.995
COLL	2284	0.002	0.998
COLL	373	0.003	0.997
COLL	379	0.003	0.997
SSHP	1379	0.996	0.004
SSHP	1523	0.998	0.002
SSHP	1824	0.998	0.002
SSHP	1921	0.998	0.002
SSHP	2040	0.997	0.003

* See Table 5 for abbreviations of canid populations.

TABLE 19A

	Canid ID	k = 4, 15 Run Average			
Canid Population^a	No.	Pop1	Pop2	Pop3	Pop4
SHIB	1769	0.9862	0.00393333	0.00473333	0.00493333
SHIB	1854	0.9806	0.0052	0.00626667	0.00793333
SHIB	1856	0.94133333	0.01373333	0.02513333	0.02
SHIB	1860	0.98093333	0.0056	0.00733333	0.00653333
SHIB	1981	0.98026667	0.00573333	0.00753333	0.00653333
CHOW	1633	0.98393333	0.00593333	0.0052	0.005
CHOW	1835	0.986	0.00473333	0.00366667	0.00546667
CHOW	1837	0.9802	0.00813333	0.00606667	0.00553333
CHOW	1838	0.98626667	0.0044	0.0048	0.0048
CHOW	1839	0.97853333	0.0088	0.00573333	0.0068
AKIT	1130	0.94546667	0.0058	0.0374	0.01133333
AKIT	1131	0.97693333	0.00486667	0.0144	0.0038
AKIT	1132	0.9882	0.00453333	0.00333333	0.00393333
AKIT	1133	0.98713333	0.00546667	0.00393333	0.00366667
AKIT	1134	0.98873333	0.00266667	0.00353333	0.00526667
AMAL	1629	0.87893333	0.06	0.0244	0.03693333
AMAL	1779	0.7818	0.01673333	0.01706667	0.1842
AMAL	1845	0.9252	0.02833333	0.02626667	0.0202
AMAL	2132	0.91766667	0.02413333	0.01786667	0.04006667
AMAL	2214	0.91493333	0.01646667	0.03	0.0388
BSJI	1338	0.7572	0.0864	0.02133333	0.1354
BSJI	1339	0.96393333	0.01353333	0.0158	0.00686667
BSJI	1645	0.97746667	0.00886667	0.00626667	0.00733333
BSJI	1675	0.95526667	0.02933333	0.00886667	0.00673333
BSJI	1717	0.97253333	0.00953333	0.00733333	0.01033333
SHAR	1573	0.95946667	0.0204	0.00653333	0.01366667
SHAR	1593	0.85086667	0.111	0.02073333	0.0172
SHAR	1619	0.90013333	0.0718	0.01546667	0.0128
SHAR	1998	0.8014	0.02793333	0.09453333	0.07633333
SHAR	1999	0.956	0.01933333	0.0078	0.01686667
HUSK	1469	0.90333333	0.02393333	0.0232	0.04973333
HUSK	1883	0.8904	0.00786667	0.07193333	0.02953333
HUSK	2115	0.77493333	0.0192	0.09933333	0.1074
HUSK	2117	0.67213333	0.027	0.1188	0.18193333
HUSK	2118	0.90086667	0.02786667	0.04093333	0.03006667
AFGH	1812	0.56573333	0.02113333	0.06673333	0.3464

TABLE 19A-continued

	Canid ID	k = 4, 15 Run Average			
Canid Population[a]	No.	Pop1	Pop2	Pop3	Pop4
AFGH	1939	0.6262	0.03553333	0.1018	0.23666667
AFGH	2264	0.55926667	0.05073333	0.0692	0.3208
AFGH	1936	0.74713333	0.05586667	0.05413333	0.14273333
AFGH	1937	0.67166667	0.0436	0.04986667	0.23486667
SALU	1491	0.4006	0.04506667	0.06466667	0.4898
SALU	1535	0.49886667	0.01166667	0.05393333	0.4354
SALU	1607	0.45526667	0.02433333	0.04333333	0.477
SALU	1873	0.2272	0.06186667	0.08613333	0.62433333
SALU	2610	0.37806667	0.0618	0.0416	0.5184
TIBT	1466	0.49693333	0.0552	0.18146667	0.26653333
TIBT	1562	0.36673333	0.1172	0.24446667	0.27173333
TIBT	1707	0.38166667	0.2034	0.04906667	0.36593333
TIBT	26078	0.43486667	0.0804	0.101	0.38373333
TIBT	28086	0.16093333	0.14593333	0.12653333	0.56666667
LHSA	1524	0.35406667	0.01493333	0.55546667	0.0756
LHSA	1525	0.44253333	0.01693333	0.4188	0.12166667
LHSA	1526	0.331	0.03193333	0.42106667	0.21606667
LHSA	1528	0.28613333	0.07026667	0.5356	0.10806667
LHSA	2074	0.59526667	0.01573333	0.28666667	0.1024
SAMO	1375	0.23546667	0.01233333	0.6444	0.1078
SAMO	1532	0.46653333	0.0064	0.48693333	0.04046667
SAMO	1560	0.51173333	0.02726667	0.37386667	0.08686667
SAMO	169	0.3968	0.0122	0.50726667	0.0838
SAMO	239	0.40986667	0.02673333	0.49193333	0.07133333
PEKE	1143	0.30666667	0.0062	0.5552	0.13173333
PEKE	1145	0.1708	0.00693333	0.60313333	0.2192
PEKE	1211	0.1872	0.0086	0.65013333	0.15393333
PEKE	1212	0.14846667	0.1002	0.59466667	0.15693333
PEKE	1213	0.23773333	0.0056	0.6136	0.14306667
SHIH	1393	0.15306667	0.08493333	0.61986667	0.14206667
SHIH	1783	0.14486667	0.00826667	0.70373333	0.14333333
SHIH	2068	0.15553333	0.0106	0.66613333	0.16773333
SHIH	2859	0.20993333	0.01053333	0.69053333	0.08913333
SHIH	2860	0.3304	0.01586667	0.40086667	0.2528
IWOF	1581	0.0168	0.3314	0.57773333	0.0742
IWOF	1761	0.00506667	0.11346667	0.66893333	0.2124
IWOF	1792	0.01426667	0.1258	0.641	0.21893333
IWOF	1906	0.01446667	0.13733333	0.70666667	0.14166667
IWOF	1993	0.00586667	0.11806667	0.65613333	0.22006667
STBD	1075	0.0306	0.2296	0.40906667	0.33073333
STBD	1714	0.01853333	0.08833333	0.6668	0.2266
STBD	1750	0.01566667	0.22233333	0.48973333	0.27226667
STBD	2403	0.00846667	0.0614	0.69553333	0.23453333
STBD	2404	0.0078	0.40166667	0.524	0.0666
GREY	2477	0.0444	0.09686667	0.765	0.0938
GREY	2478	0.01273333	0.05146667	0.75186667	0.18393333
GREY	2479	0.0094	0.17826667	0.6994	0.11306667
GREY	2480	0.01386667	0.04133333	0.8324	0.1126
GREY	2481	0.00573333	0.0872	0.65273333	0.2544
BELS	1351	0.00686667	0.0086	0.96793333	0.0168
BELS	2111	0.0314	0.00953333	0.94333333	0.0158
BELS	2153	0.00373333	0.00453333	0.98086667	0.0108
BELS	2209	0.01126667	0.0056	0.9696	0.01353333
BELS	2210	0.01166667	0.01566667	0.94853333	0.02413333
TURV	1622	0.00333333	0.0054	0.97573333	0.01573333
TURV	2194	0.01046667	0.05633333	0.799	0.13413333
TURV	2200	0.01726667	0.01913333	0.90673333	0.05713333
TURV	2222	0.00473333	0.01653333	0.84253333	0.13633333
BORZ	1378	0.05593333	0.01486667	0.7554	0.17386667
BORZ	1401	0.0358	0.03173333	0.68146667	0.25066667
BORZ	1808	0.064	0.0278	0.66526667	0.2428
BORZ	2268	0.02186667	0.0252	0.81853333	0.13446667
BORZ	978	0.0262	0.02046667	0.68133333	0.2722
COLL	1692	0.00513333	0.0512	0.718	0.22553333
COLL	1701	0.01646667	0.01206667	0.76006667	0.21133333
COLL	2284	0.0048	0.01013333	0.786	0.19926667
COLL	373	0.00393333	0.01066667	0.78246667	0.2028
COLL	379	0.00393333	0.0094	0.7856	0.20113333
SSHP	1379	0.02233333	0.19673333	0.5936	0.18726667
SSHP	1523	0.02086667	0.04446667	0.73086667	0.20373333
SSHP	1824	0.0084	0.168	0.65733333	0.16646667
SSHP	1921	0.00573333	0.08706667	0.6808	0.22633333
SSHP	2040	0.0296	0.03046667	0.7582	0.18166667
PUG	1077	0.00746667	0.0072	0.4794	0.50606667
PUG	1104	0.0188	0.0076	0.49706667	0.47646667

TABLE 19A-continued

Canid Population^a	Canid ID No.	k = 4, 15 Run Average Pop1	Pop2	Pop3	Pop4
PUG	1183	0.07146667	0.01226667	0.4226	0.49393333
PUG	1184	0.0082	0.00713333	0.495	0.48966667
PUG	1192	0.006	0.05273333	0.438	0.50326667
KOMO	1484	0.02893333	0.08226667	0.29953333	0.5892
KOMO	1964	0.03166667	0.1022	0.2362	0.63
KOMO	2321	0.04006667	0.13546667	0.2222	0.6022
KOMO	2323	0.08526667	0.10286667	0.14026667	0.67173333
KOMO	2334	0.00913333	0.08426667	0.1342	0.77246667
WHIP	1355	0.0062	0.05526667	0.4162	0.52246667
WHIP	1395	0.00873333	0.09993333	0.4982	0.39313333
WHIP	1407	0.00713333	0.12913333	0.30046667	0.56313333
WHIP	1409	0.00566667	0.05026667	0.72593333	0.218
WHIP	1518	0.0056	0.10146667	0.45786667	0.435
SPOO	1530	0.05693333	0.25666667	0.36106667	0.3252
SPOO	1582	0.07346667	0.11826667	0.38393333	0.42473333
SPOO	1876	0.0106	0.12953333	0.50726667	0.35246667
SPOO	1877	0.0136	0.16693333	0.37186667	0.44753333
SPOO	2337	0.00593333	0.0468	0.2268	0.7206
BICH	1943	0.0758	0.0702	0.35546667	0.4986
BICH	1954	0.14973333	0.05386667	0.31746667	0.47873333
BICH	933	0.03653333	0.1844	0.31173333	0.46746667
BICH	974	0.07046667	0.0902	0.29946667	0.53993333
KEES	1501	0.03973333	0.03486667	0.5276	0.39786667
KEES	1589	0.00533333	0.03853333	0.44706667	0.5092
KEES	1818	0.02126667	0.0422	0.4594	0.47733333
KEES	1819	0.00526667	0.0386	0.54426667	0.41153333
KEES	2072	0.0064	0.06153333	0.4162	0.51586667
MNTY	1539	0.01293333	0.2696	0.13173333	0.5856
MNTY	1732	0.0262	0.15633333	0.1496	0.66773333
MNTY	2145	0.01133333	0.20213333	0.35033333	0.4362
MNTY	2149	0.01066667	0.06813333	0.57466667	0.34666667
NELK	2216	0.05673333	0.1076	0.30873333	0.52693333
NELK	2239	0.18626667	0.03333333	0.4914	0.289
NELK	2240	0.02666667	0.1904	0.44286667	0.34013333
NELK	2281	0.012	0.0752	0.10806667	0.80493333
NELK	2295	0.24066667	0.04506667	0.29186667	0.42233333
KUVZ	1482	0.0566	0.0156	0.52573333	0.4018
KUVZ	1551	0.18713333	0.02206667	0.41506667	0.3758
KUVZ	1672	0.07186667	0.05426667	0.20386667	0.66993333
KUVZ	1913	0.02453333	0.06113333	0.34526667	0.56926667
KUVZ	1994	0.04446667	0.06193333	0.40193333	0.49186667
DANE	1574	0.01126667	0.086	0.17386667	0.72873333
DANE	1575	0.1096	0.12853333	0.19233333	0.5696
DANE	1580	0.0112	0.0698	0.21413333	0.705
DANE	1700	0.00773333	0.06426667	0.41106667	0.51706667
DANE	1748	0.19526667	0.07813333	0.20826667	0.51826667
WSSP	1955	0.00506667	0.0726	0.3252	0.59726667
WSSP	2139	0.01333333	0.0658	0.24086667	0.67993333
WSSP	2143	0.00386667	0.07613333	0.20346667	0.71646667
WSSP	2195	0.0078	0.10353333	0.29773333	0.59093333
WSSP	2286	0.0054	0.09933333	0.20973333	0.68546667
DOBP	1031	0.007	0.08406667	0.18426667	0.7248
DOBP	1032	0.03506667	0.09113333	0.1938	0.68006667
DOBP	1749	0.01766667	0.17506667	0.19726667	0.60986667
DOBP	2162	0.00786667	0.08273333	0.19973333	0.70986667
DOBP	2245	0.0054	0.0814	0.1972	0.71593333
SSNZ	13352	0.00353333	0.26246667	0.1206	0.61326667
SSNZ	1360	0.00353333	0.12506667	0.1222	0.74906667
SSNZ	1827	0.00653333	0.092	0.19446667	0.70726667
SSNZ	20457	0.0084	0.07666667	0.22706667	0.6882
SSNZ	22647	0.00753333	0.18713333	0.16033333	0.64526667
ITGY	1568	0.03193333	0.076	0.1174	0.77473333
ITGY	1570	0.01333333	0.0768	0.0818	0.82806667
ITGY	1862	0.10826667	0.06413333	0.08133333	0.74633333
ITGY	1881	0.042	0.06533333	0.0726	0.82
ITGY	1882	0.172	0.05926667	0.12893333	0.6398
OES	1984	0.0208	0.0792	0.06466667	0.83533333
OES	2171	0.0094	0.07693333	0.17926667	0.7344
OES	2179	0.01033333	0.08166667	0.1854	0.72273333
OES	1914	0.02013333	0.12153333	0.10093333	0.75773333
OES	2626	0.05893333	0.0684	0.0808	0.79173333
AMWS	2168	0.01106667	0.07626667	0.16186667	0.7508
AMWS	2279	0.01213333	0.13833333	0.1118	0.73766667
AMWS	2327	0.06306667	0.14373333	0.07946667	0.71366667
AMWS	987	0.0132	0.09766667	0.17166667	0.71766667

TABLE 19A-continued

	Canid ID	k = 4, 15 Run Average			
Canid Population[a]	No.	Pop1	Pop2	Pop3	Pop4
AMWS	988	0.0164	0.17813333	0.12913333	0.6764
MSNZ	1587	0.00553333	0.15366667	0.11553333	0.72533333
MSNZ	1756	0.00593333	0.07446667	0.16326667	0.75586667
MSNZ	1851	0.00406667	0.09013333	0.1284	0.77753333
MSNZ	2034	0.026	0.2376	0.1144	0.62193333
MSNZ	2613	0.00513333	0.12266667	0.12486667	0.74726667
AUST	1387	0.04046667	0.11066667	0.20053333	0.6482
AUST	1531	0.0178	0.139	0.06606667	0.77713333
AUST	1564	0.00726667	0.0902	0.0582	0.8444
AUST	1870	0.0388	0.1046	0.13213333	0.7246
AUST	1871	0.00673333	0.0902	0.06326667	0.84006667
ECKR	1376	0.004	0.11126667	0.0808	0.8038
ECKR	1377	0.00406667	0.08373333	0.14606667	0.76593333
ECKR	1400	0.0034	0.06993333	0.26133333	0.66546667
ECKR	1404	0.0034	0.09186667	0.23986667	0.66486667
ECKR	1511	0.0068	0.08413333	0.18326667	0.72573333
IRSE	1540	0.00333333	0.0736	0.08586667	0.83726667
IRSE	1617	0.0038	0.072	0.07486667	0.8494
IRSE	1896	0.00906667	0.07533333	0.11866667	0.79666667
IRSE	2084	0.00406667	0.06606667	0.2228	0.70706667
IRSE	2085	0.00326667	0.0842	0.0818	0.831
WHWT	1388	0.0142	0.0704	0.05473333	0.86053333
WHWT	1420	0.0452	0.0842	0.08166667	0.7888
WHWT	1992	0.0108	0.08613333	0.07613333	0.82693333
WHWT	2100	0.01053333	0.0824	0.04333333	0.86353333
WHWT	2128	0.0158	0.0728	0.03166667	0.87973333
PNTR	1382	0.00826667	0.07166667	0.07566667	0.8442
PNTR	1383	0.01426667	0.07086667	0.0714	0.84353333
PNTR	1869	0.00726667	0.0582	0.12293333	0.81146667
PNTR	1938	0.0098	0.07566667	0.15733333	0.75693333
PNTR	1948	0.05646667	0.0598	0.0958	0.78773333
BASS	1341	0.02966667	0.1016	0.04426667	0.82446667
BASS	1342	0.01053333	0.0758	0.09866667	0.81473333
BASS	1506	0.0078	0.08493333	0.0752	0.8318
BASS	1917	0.00926667	0.10106667	0.04406667	0.84593333
CKCS	1513	0.0408	0.0656	0.12133333	0.77233333
CKCS	1639	0.00753333	0.07806667	0.12053333	0.794
CKCS	1640	0.00806667	0.0998	0.1152	0.77686667
CKCS	1642	0.0048	0.07466667	0.13413333	0.78653333
CKCS	2054	0.00553333	0.07133333	0.1202	0.80293333
GSNZ	1868	0.27746667	0.06873333	0.06233333	0.5912
GSNZ	22739	0.1848	0.06566667	0.06806667	0.68133333
GSNZ	27093	0.05206667	0.08053333	0.06046667	0.807
GSNZ	27106	0.0098	0.10226667	0.0224	0.8656
GSNZ	33390	0.0082	0.09093333	0.0874	0.81346667
PHAR	1292	0.12533333	0.05726667	0.0088	0.80886667
PHAR	1947	0.1386	0.05446667	0.01913333	0.78773333
PHAR	1962	0.13706667	0.0674	0.06313333	0.7326
PHAR	1963	0.10473333	0.0708	0.012	0.81246667
GOLD	591	0.00453333	0.15633333	0.02266667	0.8164
GOLD	592	0.02186667	0.2448	0.0112	0.72213333
GOLD	593	0.00693333	0.1734	0.01473333	0.80526667
GOLD	603	0.0058	0.148	0.009	0.83726667
GOLD	604	0.00386667	0.19653333	0.03653333	0.76313333
BEAG	1323	0.012	0.169	0.01126667	0.80753333
BEAG	1324	0.01733333	0.09226667	0.126	0.7644
BEAG	1327	0.00813333	0.2708	0.0204	0.70093333
BEAG	994	0.029	0.25213333	0.06993333	0.64906667
BEAG	995	0.01573333	0.0918	0.06013333	0.83213333
BLDH	1186	0.0088	0.224	0.0264667	0.7406
BLDH	1223	0.0126	0.15126667	0.01466667	0.82126667
BLDH	1410	0.0056	0.3068	0.00726667	0.68026667
BLDH	1942	0.00893333	0.17273333	0.00906667	0.80933333
BLDH	1957	0.00693333	0.16	0.01146667	0.82153333
AIRT	1603	0.03993333	0.15466667	0.11033333	0.69526667
AIRT	1604	0.00613333	0.08966667	0.12693333	0.7772
AIRT	1788	0.00466667	0.20253333	0.09266667	0.70013333
AIRT	1875	0.01793333	0.09733333	0.13313333	0.7516
ACKR	1035	0.0102	0.09006667	0.08406667	0.8156
ACKR	2261	0.02313333	0.0972	0.1014	0.77833333
ACKR	2310	0.0038	0.09926667	0.026	0.87086667
ACKR	1956	0.00913333	0.1278	0.02146667	0.84173333
ACKR	2260	0.00533333	0.10193333	0.03026667	0.86233333
AHRT	1120	0.00986667	0.12326667	0.0524	0.8144
AHRT	1121	0.0104	0.18726667	0.04926667	0.753

TABLE 19A-continued

	Canid ID	k = 4, 15 Run Average			
Canid Population[a]	No.	Pop1	Pop2	Pop3	Pop4
AHRT	1122	0.00853333	0.1532	0.089	0.74886667
AHRT	1123	0.00866667	0.14433333	0.07606667	0.77093333
AHRT	1124	0.0076	0.1374	0.05166667	0.80346667
CHBR	1546	0.01113333	0.13993333	0.05573333	0.7932
CHBR	1549	0.06426667	0.33173333	0.01326667	0.5908
CHBR	1813	0.00446667	0.17893333	0.02786667	0.7888
CHBR	2091	0.0086	0.1008	0.038	0.85266667
CHBR	888	0.00506667	0.11486667	0.02473333	0.8552
CAIR	1405	0.00846667	0.277	0.0828	0.6316
CAIR	2096	0.0146	0.07973333	0.03353333	0.87213333
CAIR	2113	0.01413333	0.1012	0.10746667	0.77733333
CAIR	2125	0.0062	0.0752	0.07646667	0.8422
CAIR	2131	0.0292	0.08106667	0.0632	0.82666667
PTWD	P142	0.0074	0.1588	0.11633333	0.71733333
PTWD	P1	0.00453333	0.192	0.1194	0.68413333
PTWD	P238	0.01333333	0.1686	0.17253333	0.64566667
PTWD	P25	0.00413333	0.07453333	0.1428	0.77853333
PTWD	P67	0.00613333	0.07766667	0.1434	0.77266667
GSHP	1628	0.00506667	0.13306667	0.08306667	0.77886667
GSHP	1708	0.02013333	0.08246667	0.20713333	0.69033333
GSHP	1710	0.02533333	0.08533333	0.072	0.8172
GSHP	1833	0.00806667	0.44793333	0.03073333	0.5134
GSHP	1892	0.01533333	0.1122	0.07586667	0.79673333
BORD	1648	0.11253333	0.07173333	0.0404	0.77573333
BORD	1828	0.01326667	0.07473333	0.09166667	0.82006667
BORD	1829	0.00546667	0.24266667	0.13626667	0.61566667
BORD	2002	0.01993333	0.10706667	0.12306667	0.75
BORD	2003	0.03286667	0.08433333	0.11186667	0.77086667
BEDT	1422	0.00793333	0.32966667	0.12893333	0.5334
BEDT	1423	0.00626667	0.1544	0.15853333	0.68086667
BEDT	1424	0.01353333	0.12806667	0.2118	0.64666667
BEDT	1426	0.0142	0.2006	0.16206667	0.62333333
CLSP	1008	0.00746667	0.3506	0.06153333	0.5802
CLSP	1009	0.00386667	0.316	0.075	0.60473333
CLSP	1802	0.00646667	0.32126667	0.07473333	0.59733333
CLSP	2312	0.00413333	0.3918	0.06026667	0.5438
CLSP	2314	0.00473333	0.395	0.06026667	0.53973333
IBIZ	1147	0.0094	0.09326667	0.0498	0.84746667
IBIZ	1148	0.0076	0.2762	0.12373333	0.59233333
IBIZ	1162	0.00813333	0.07513333	0.0816	0.8354
IBIZ	1172	0.02393333	0.09233333	0.1424	0.7416
IBIZ	1280	0.027	0.20926667	0.20173333	0.56186667
RHOD	1444	0.0056	0.13373333	0.17626667	0.68426667
RHOD	1454	0.02113333	0.17686667	0.17033333	0.63213333
RHOD	1505	0.01006667	0.11066667	0.0728	0.80653333
RHOD	1592	0.00833333	0.4782	0.06833333	0.44506667
RHOD	1609	0.00606667	0.1752	0.2602	0.55853333
DACH	1051	0.01053333	0.25333333	0.23673333	0.49933333
DACH	1052	0.00893333	0.2756	0.21553333	0.49993333
DACH	1053	0.0174	0.33433333	0.12966667	0.5186
DACH	1054	0.02753333	0.43573333	0.13406667	0.40273333
DACH	1055	0.00966667	0.27553333	0.24213333	0.47253333
AUSS	1336	0.19213333	0.16606667	0.19266667	0.449
AUSS	1337	0.01626667	0.218	0.16453333	0.60106667
AUSS	1500	0.00893333	0.06726667	0.2208	0.70266667
AUSS	1521	0.11106667	0.43073333	0.18213333	0.27613333
AUSS	1683	0.01366667	0.2222	0.091	0.67313333
CHIH	1202	0.0064	0.22773333	0.1	0.66586667
CHIH	1203	0.0148	0.09106667	0.30626667	0.58766667
CHIH	1204	0.01226667	0.12713333	0.14806667	0.71253333
CHIH	1205	0.0992	0.32273333	0.15366667	0.42466667
CHIH	1206	0.0062	0.37573333	0.09806667	0.51986667
KERY	13878	0.00706667	0.22393333	0.15313333	0.61586667
KERY	1483	0.00713333	0.2578	0.16	0.57506667
KERY	1579	0.0126	0.10493333	0.18953333	0.69286667
KERY	2014	0.0036	0.342	0.07906667	0.5752
KERY	24255	0.00853333	0.35613333	0.15386667	0.48133333
SCHP	1386	0.0076	0.19293333	0.036	0.76353333
SCHP	1471	0.00766667	0.20733333	0.02273333	0.76213333
SCHP	1814	0.01046667	0.289	0.0824	0.6182
SCHP	1852	0.0162	0.13586667	0.15466667	0.69326667
IRTR	2152	0.01113333	0.14993333	0.093	0.746
IRTR	2189	0.01146667	0.36666667	0.08746667	0.53433333
IRTR	2238	0.0052	0.36626667	0.043	0.58546667
IRTR	2242	0.00893333	0.27573333	0.06926667	0.64613333

TABLE 19A-continued

	Canid ID	k = 4, 15 Run Average			
Canid Population[a]	No.	Pop1	Pop2	Pop3	Pop4
FCR	1188	0.0062	0.22606667	0.05746667	0.7102
FCR	2020	0.00506667	0.1566	0.08913333	0.749
FCR	2042	0.0048	0.23086667	0.0638	0.70053333
FCR	2044	0.00613333	0.17806667	0.16073333	0.65506667
FCR	2259	0.0036	0.24293333	0.048	0.70526667
SCWT	1624	0.0506	0.4248	0.08933333	0.4352
SCWT	1770	0.00433333	0.2824	0.31153333	0.40166667
SCWT	2250	0.00513333	0.22033333	0.04646667	0.7282
SCWT	2301	0.0162	0.36513333	0.03973333	0.57913333
POM	1190	0.09806667	0.35386667	0.32793333	0.22
POM	1191	0.00926667	0.7472	0.04853333	0.19473333
POM	1210	0.04093333	0.3494	0.1288	0.48053333
POM	1238	0.00613333	0.16306667	0.26906667	0.56173333
POM	1239	0.1202	0.08513333	0.2394	0.555
LAB	1310	0.11153333	0.54806667	0.0612	0.2794
LAB	1465	0.01346667	0.33846667	0.05966667	0.5884
LAB	1468	0.02113333	0.40553333	0.09626667	0.477
LAB	1754	0.01206667	0.6368	0.01	0.34093333
LAB	1830	0.00533333	0.5134	0.14593333	0.33526667
PRES	1082	0.00793333	0.73346667	0.0294	0.22913333
PRES	1096	0.00493333	0.7488	0.05413333	0.19193333
PRES	1115	0.00993333	0.64406667	0.086	0.2604
PRES	1127	0.10286667	0.85446667	0.01946667	0.0234
PRES	1095	0.05353333	0.82886667	0.03246667	0.08533333
ROTT	1014	0.01153333	0.72453333	0.13553333	0.12833333
ROTT	1028	0.00553333	0.712	0.13746667	0.1448
ROTT	1029	0.0042	0.8398	0.05386667	0.10193333
ROTT	1033	0.006	0.85826667	0.04853333	0.08746667
ROTT	1034	0.00453333	0.85426667	0.11393333	0.02726667
BULM	1105	0.0056	0.94446667	0.01333333	0.03626667
BULM	1106	0.00486667	0.61486667	0.0896	0.2908
BULM	1107	0.01853333	0.90133333	0.026	0.05413333
BULM	1108	0.00653333	0.93873333	0.02386667	0.03073333
BULM	1109	0.00513333	0.96613333	0.00746667	0.0212
NEWF	271	0.0132	0.866	0.0532	0.0676
NEWF	274	0.00526667	0.94806667	0.00966667	0.03706667
NEWF	275	0.00733333	0.97226667	0.0052	0.01533333
NEWF	277	0.00586667	0.97893333	0.00673333	0.00833333
NEWF	278	0.06706667	0.8476	0.01493333	0.07053333
GSD	1666	0.00613333	0.88413333	0.08013333	0.02946667
GSD	1776	0.00306667	0.89873333	0.07173333	0.0264
GSD	2011	0.00773333	0.853	0.0962	0.04313333
GSD	2060	0.00613333	0.81526667	0.10273333	0.07626667
GSD	2086	0.00573333	0.84086667	0.10013333	0.05313333
FBUL	1507	0.0104	0.96366667	0.0158	0.00986667
FBUL	1508	0.00626667	0.96013333	0.01466667	0.0188
FBUL	1509	0.00493333	0.97453333	0.0106	0.01006667
FBUL	2671	0.01693333	0.91053333	0.01173333	0.0608
MBLT	1915	0.00553333	0.9154	0.008	0.071
MBLT	2253	0.0068	0.89166667	0.045	0.0564
MBLT	2254	0.036	0.9132	0.03073333	0.02006667
MBLT	2255	0.0098	0.90326667	0.00946667	0.0772
MBLT	2256	0.0062	0.97946667	0.00573333	0.0086
BULD	1193	0.01906667	0.95466667	0.01473333	0.01153333
BULD	1194	0.00513333	0.9824	0.00626667	0.00593333
BULD	1195	0.0036	0.98433333	0.00473333	0.00726667
BULD	1197	0.0052	0.92026667	0.05506667	0.0194
BULD	1198	0.00553333	0.96853333	0.0138	0.01206667
BOX	1176	0.00313333	0.91446667	0.07333333	0.009
BOX	1177	0.00366667	0.92693333	0.05286667	0.01653333
BOX	1178	0.00446667	0.93326667	0.05726667	0.00513333
BOX	1179	0.00233333	0.92526667	0.06886667	0.0036
BOX	1304	0.00266667	0.9162	0.07473333	0.00593333
MAST	1015	0.004	0.9386	0.0162	0.04126667
MAST	1016	0.009	0.90766667	0.06406667	0.01933333
MAST	1017	0.0046	0.9216	0.0498	0.024
MAST	1066	0.0158	0.94853333	0.018	0.01753333
MAST	991	0.01866667	0.95213333	0.0108	0.0186
BMD	941	0.00406667	0.76213333	0.21013333	0.02386667
BMD	943	0.0094	0.58306667	0.2496	0.1578
BMD	968	0.0062	0.74973333	0.21286667	0.03113333
BMD	1763	0.0046	0.74813333	0.20066667	0.04646667
BMD	969	0.00373333	0.69866667	0.2714	0.02653333
GSMD	1547	0.0066	0.41546667	0.36546667	0.21266667
GSMD	1659	0.0052	0.5908	0.34013333	0.0638

TABLE 19A-continued

Canid Population[a]	Canid ID No.	k = 4, 15 Run Average			
		Pop1	Pop2	Pop3	Pop4
GSMD	1660	0.013	0.41086667	0.435	0.14126667
GSMD	1662	0.04386667	0.51266667	0.304	0.13973333
GSMD	1663	0.00653333	0.50973333	0.42086667	0.063

TABLE 19B

Canid Population[a]	Canid ID No.	k = 3, 15 Run Average		
		Pop1	Pop2	Pop3
SHIB	1769	0.989667	0.004667	0.005667
SHIB	1854	0.982933	0.006867	0.0102
SHIB	1856	0.9584	0.016067	0.025667
SHIB	1860	0.9852	0.0066	0.008267
SHIB	1981	0.983733	0.0078	0.008133
CHOW	1633	0.985533	0.008133	0.0064
CHOW	1835	0.988133	0.006133	0.0058
CHOW	1837	0.982067	0.0094	0.0084
CHOW	1838	0.9884	0.0056	0.006
CHOW	1839	0.978667	0.0116	0.009867
AKIT	1130	0.9576	0.007467	0.035
AKIT	1131	0.988933	0.0052	0.005733
AKIT	1132	0.989133	0.005867	0.004933
AKIT	1133	0.988133	0.0072	0.004667
AKIT	1134	0.991	0.003667	0.005467
AMAL	1629	0.8604	0.083867	0.055733
AMAL	1779	0.7986	0.020667	0.1806
AMAL	1845	0.9078	0.047	0.045067
AMAL	2132	0.920333	0.0362	0.043533
AMAL	2214	0.908333	0.0218	0.069733
BSJI	1338	0.762067	0.122333	0.1156
BSJI	1339	0.973267	0.018	0.0088
BSJI	1645	0.977733	0.012933	0.009467
BSJI	1675	0.945333	0.0468	0.007933
BSJI	1717	0.972533	0.013667	0.013867
SHAR	1573	0.9602	0.028267	0.0116
SHAR	1593	0.845667	0.138	0.016533
SHAR	1619	0.870933	0.1136	0.015467
SHAR	1998	0.7902	0.031533	0.178267
SHAR	1999	0.957	0.029067	0.014
HUSK	1469	0.915533	0.037133	0.0474
HUSK	1883	0.907867	0.0104	0.0818
HUSK	2115	0.748733	0.013533	0.237867
HUSK	2117	0.632333	0.013333	0.3544
HUSK	2118	0.905133	0.042133	0.052533
AFGH	1812	0.601933	0.0432	0.3548
AFGH	1939	0.6604	0.084067	0.255467
AFGH	2264	0.6198	0.122933	0.2574
AFGH	1936	0.785067	0.0934	0.121467
AFGH	1937	0.717867	0.070933	0.2112
SALU	1491	0.4102	0.017667	0.5722
SALU	1535	0.542067	0.007067	0.450867
SALU	1607	0.500067	0.020533	0.479467
SALU	1873	0.292667	0.031667	0.675733
SALU	2610	0.4434	0.055533	0.501
TIBT	1466	0.479867	0.027867	0.492333
TIBT	1562	0.355667	0.0502	0.594
TIBT	1707	0.397133	0.240333	0.362333
TIBT	26078	0.431867	0.0466	0.521533
TIBT	28086	0.163267	0.103733	0.733067
LHSA	1524	0.558933	0.034333	0.4066
LHSA	1525	0.5262	0.023	0.451
LHSA	1526	0.463467	0.020533	0.5162
LHSA	1528	0.3624	0.0748	0.562667
LHSA	2074	0.705	0.023	0.272067
SAMO	1375	0.271267	0.011733	0.716867
SAMO	1532	0.553067	0.0086	0.438267
SAMO	1560	0.5902	0.0374	0.372533
SAMO	169	0.436867	0.016867	0.546267
SAMO	239	0.458933	0.038267	0.502867
PEKE	1143	0.696267	0.013267	0.2904
PEKE	1145	0.445133	0.011533	0.543333
PEKE	1211	0.457267	0.010667	0.532133
PEKE	1212	0.380333	0.2828	0.336733
PEKE	1213	0.61	0.012933	0.377067
SHIH	1393	0.390067	0.1362	0.473867
SHIH	1783	0.3624	0.011267	0.626333
SHIH	2068	0.379533	0.009533	0.610867
SHIH	2859	0.4456	0.0228	0.531667
SHIH	2860	0.5422	0.0238	0.433933
IWOF	1581	0.0226	0.2552	0.7222
IWOF	1761	0.0088	0.020333	0.970733
IWOF	1792	0.026267	0.069467	0.904467
IWOF	1906	0.052267	0.033933	0.914
IWOF	1993	0.007267	0.026733	0.966067
STBD	1075	0.0464	0.139933	0.813733
STBD	1714	0.059	0.030333	0.910733
STBD	1750	0.047733	0.2466	0.705533
STBD	2403	0.013333	0.0294	0.9572
STBD	2404	0.0206	0.376867	0.602533
GREY	2477	0.1562	0.0356	0.808267
GREY	2478	0.017867	0.018267	0.963733
GREY	2479	0.0112	0.063333	0.925333
GREY	2480	0.059467	0.011467	0.929067
GREY	2481	0.009133	0.02	0.970867
BELS	1351	0.0132	0.007333	0.979467
BELS	2111	0.0744	0.013133	0.912267
BELS	2153	0.0058	0.006067	0.988
BELS	2209	0.031467	0.005733	0.962933
BELS	2210	0.034733	0.026267	0.938867
TURV	1622	0.009067	0.010133	0.980667
TURV	2194	0.013067	0.057467	0.929333
TURV	2200	0.020267	0.010467	0.969133
TURV	2222	0.0056	0.009133	0.985133
BORZ	1378	0.136	0.007733	0.856333
BORZ	1401	0.114733	0.024133	0.861133
BORZ	1808	0.1772	0.014467	0.8084
BORZ	2268	0.063467	0.015867	0.920867
BORZ	978	0.042	0.014733	0.9434
COLL	1692	0.011933	0.020667	0.9674
COLL	1701	0.0218	0.011	0.967
COLL	2284	0.0116	0.021867	0.9666
COLL	373	0.008933	0.013	0.977933
COLL	379	0.0058	0.011267	0.9828
SSHP	1379	0.032667	0.1834	0.783933
SSHP	1523	0.050067	0.043333	0.9064
SSHP	1824	0.016067	0.141133	0.842867
SSHP	1921	0.0062	0.118733	0.875
SSHP	2040	0.08	0.152	0.768133
PUG	1077	0.010667	0.008933	0.9804
PUG	1104	0.048267	0.017733	0.933933
PUG	1183	0.121733	0.0116	0.866667
PUG	1184	0.013467	0.011733	0.975
PUG	1192	0.009333	0.098867	0.8916
KOMO	1484	0.035	0.041867	0.923067
KOMO	1964	0.036133	0.055333	0.908333
KOMO	2321	0.036	0.099533	0.8644
KOMO	2323	0.086267	0.096333	0.817467
KOMO	2334	0.0092	0.036467	0.9544
WHIP	1355	0.006867	0.0162	0.9768
WHIP	1395	0.010667	0.0362	0.953067
WHIP	1407	0.0076	0.073267	0.9192

TABLE 19B-continued

Canid Population^a	Canid ID No.	k = 3, 15 Run Average		
		Pop1	Pop2	Pop3
WHIP	1409	0.006333	0.014267	0.9794
WHIP	1518	0.005933	0.039267	0.9546
SPOO	1530	0.0676	0.185267	0.747067
SPOO	1582	0.0744	0.064333	0.8612
SPOO	1876	0.015	0.155	0.830067
SPOO	1877	0.018467	0.190133	0.791333
SPOO	2337	0.006867	0.016533	0.976667
BICH	1943	0.0654	0.019933	0.9146
BICH	1954	0.239867	0.018	0.741933
BICH	933	0.050933	0.159467	0.789467
BICH	974	0.109533	0.092333	0.798067
KEES	1501	0.060867	0.013067	0.925933
KEES	1589	0.006467	0.007267	0.986267
KEES	1818	0.015467	0.027133	0.9572
KEES	1819	0.007133	0.012733	0.980067
KEES	2072	0.008	0.0212	0.970667
MNTY	1539	0.0138	0.264733	0.7214
MNTY	1732	0.0298	0.1218	0.8486
MNTY	2145	0.014333	0.155133	0.830333
MNTY	2149	0.010533	0.014533	0.974933
NELK	2216	0.0872	0.0802	0.832467
NELK	2239	0.214533	0.02	0.765467
NELK	2240	0.0426	0.1888	0.768667
NELK	2281	0.0142	0.027533	0.958333
NELK	2295	0.293	0.025867	0.681467
KUVZ	1482	0.0854	0.0086	0.906
KUVZ	1551	0.198533	0.008533	0.793
KUVZ	1672	0.075467	0.032267	0.8924
KUVZ	1913	0.033333	0.073267	0.8936
KUVZ	1994	0.0498	0.042467	0.907867
DANE	1574	0.016533	0.026467	0.957
DANE	1575	0.1558	0.1312	0.713
DANE	1580	0.011	0.007067	0.982
DANE	1700	0.0088	0.016933	0.9742
DANE	1748	0.1982	0.034533	0.767333
WSSP	1955	0.0066	0.015867	0.977533
WSSP	2139	0.018667	0.028867	0.952533
WSSP	2143	0.0056	0.033333	0.961133
WSSP	2195	0.014467	0.065667	0.920133
WSSP	2286	0.007133	0.102133	0.890867
DOBP	1031	0.012667	0.102067	0.8852
DOBP	1032	0.047733	0.092733	0.859267
DOBP	1749	0.0394	0.2362	0.724467
DOBP	2162	0.013133	0.0862	0.9008
DOBP	2245	0.008467	0.085933	0.9056
SSNZ	13352	0.004733	0.290333	0.705133
SSNZ	1360	0.004267	0.093667	0.902133
SSNZ	1827	0.007067	0.034467	0.958533
SSNZ	20457	0.009267	0.021267	0.969267
SSNZ	22647	0.0088	0.203333	0.7878
ITGY	1568	0.022933	0.012267	0.965067
ITGY	1570	0.019333	0.061067	0.919533
ITGY	1862	0.1134	0.021067	0.865533
ITGY	1881	0.0564	0.017467	0.9262
ITGY	1882	0.1768	0.014467	0.808667
OES	1984	0.022133	0.022067	0.955667
OES	2171	0.009	0.028867	0.962067
OES	2179	0.011267	0.022	0.966867
OES	1914	0.020467	0.0566	0.9232
OES	2626	0.062467	0.013267	0.924333
AMWS	2168	0.012	0.020333	0.967667
AMWS	2279	0.012	0.195533	0.792467
AMWS	2327	0.0978	0.257667	0.6446
AMWS	987	0.018933	0.108533	0.8722
AMWS	988	0.019667	0.155133	0.825333
MSNZ	1587	0.0078	0.129067	0.8634
MSNZ	1756	0.006733	0.011	0.9824
MSNZ	1851	0.005067	0.029733	0.9652
MSNZ	2034	0.0352	0.1964	0.7686
MSNZ	2613	0.0062	0.0746	0.919333
AUST	1387	0.046333	0.052533	0.9012
AUST	1531	0.0178	0.145467	0.836933
AUST	1564	0.008067	0.045867	0.946
AUST	1870	0.051933	0.069333	0.878667
AUST	1871	0.008533	0.072	0.9196
ECKR	1376	0.005467	0.0664	0.928
ECKR	1377	0.005133	0.032267	0.962333
ECKR	1400	0.003867	0.036667	0.9594
ECKR	1404	0.004067	0.042933	0.952867
ECKR	1511	0.008333	0.081333	0.910267
IRSE	1540	0.0042	0.0116	0.984133
IRSE	1617	0.005267	0.010867	0.9838
IRSE	1896	0.009267	0.017133	0.9736
IRSE	2084	0.004333	0.008133	0.9876
IRSE	2085	0.004267	0.029467	0.966067
WHWT	1388	0.013	0.013667	0.973533
WHWT	1420	0.037133	0.0254	0.937267
WHWT	1992	0.0094	0.02	0.970867
WHWT	2100	0.009933	0.033333	0.956667
WHWT	2128	0.011533	0.009467	0.979
PNTR	1382	0.0116	0.0096	0.978867
PNTR	1383	0.025867	0.019933	0.9542
PNTR	1869	0.011667	0.007867	0.980533
PNTR	1938	0.010867	0.015533	0.973667
PNTR	1948	0.066533	0.008533	0.925
BASS	1341	0.035333	0.0746	0.890067
BASS	1342	0.014067	0.015467	0.970533
BASS	1506	0.008467	0.045133	0.946533
BASS	1917	0.0118	0.065067	0.923133
CKCS	1513	0.039067	0.011467	0.949533
CKCS	1639	0.0096	0.034067	0.956267
CKCS	1640	0.011467	0.1124	0.875867
CKCS	1642	0.008133	0.017133	0.9748
CKCS	2054	0.0076	0.014533	0.977733
GSNZ	1868	0.2806	0.028467	0.691
GSNZ	22739	0.187	0.026133	0.787
GSNZ	27093	0.064533	0.027667	0.9078
GSNZ	27106	0.0126	0.0828	0.9048
GSNZ	33390	0.011667	0.053533	0.9348
PHAR	1292	0.152867	0.015267	0.831867
PHAR	1947	0.207067	0.007933	0.785067
PHAR	1962	0.1676	0.0442	0.788333
PHAR	1963	0.142533	0.021667	0.8358
GOLD	591	0.006467	0.268667	0.724933
GOLD	592	0.0284	0.465467	0.506067
GOLD	593	0.007867	0.295733	0.696533
GOLD	603	0.0082	0.3306	0.6614
GOLD	604	0.004533	0.283333	0.712267
BEAG	1323	0.012467	0.292	0.695667
BEAG	1324	0.019267	0.052133	0.928667
BEAG	1327	0.008867	0.3602	0.630667
BEAG	994	0.0326	0.3418	0.625467
BEAG	995	0.026333	0.1152	0.858467
BLDH	1186	0.014133	0.626733	0.358933
BLDH	1223	0.017133	0.404467	0.578267
BLDH	1410	0.006467	0.772733	0.2208
BLDH	1942	0.013	0.5678	0.419333
BLDH	1957	0.008933	0.458133	0.532733
AIRT	1603	0.059733	0.2394	0.701067
AIRT	1604	0.008533	0.090133	0.901467
AIRT	1788	0.006533	0.4282	0.5652
AIRT	1875	0.022733	0.1192	0.857867
ACKR	1035	0.014333	0.040733	0.944933
ACKR	2261	0.0278	0.050867	0.921333
ACKR	2310	0.004867	0.061133	0.9338
ACKR	1956	0.0142	0.155667	0.830267
ACKR	2260	0.006867	0.077	0.915867
AHRT	1120	0.016333	0.104	0.879467
AHRT	1121	0.013733	0.185067	0.801267
AHRT	1122	0.0096	0.190467	0.8002
AHRT	1123	0.0118	0.097333	0.891
AHRT	1124	0.0106	0.091933	0.8974
CHBR	1546	0.013133	0.096333	0.890667
CHBR	1549	0.0814	0.445533	0.473
CHBR	1813	0.0054	0.23	0.7646
CHBR	2091	0.0118	0.073267	0.915
CHBR	888	0.0056	0.118533	0.876
CAIR	1405	0.01	0.289333	0.7004
CAIR	2096	0.022667	0.041733	0.935533
CAIR	2113	0.0158	0.050867	0.933333

TABLE 19B-continued

Canid	Canid	k = 3, 15 Run Average		
Population[a]	ID No.	Pop1	Pop2	Pop3
CAIR	2125	0.006333	0.0114	0.9824
CAIR	2131	0.0202	0.027533	0.952333
PTWD	P142	0.007067	0.1418	0.8512
PTWD	P1	0.005067	0.2378	0.757
PTWD	P238	0.0172	0.209333	0.773467
PTWD	P25	0.005133	0.021667	0.9732
PTWD	P67	0.007067	0.023	0.97
GSHP	1628	0.006533	0.155933	0.837533
GSHP	1708	0.042867	0.041333	0.915867
GSHP	1710	0.0406	0.0372	0.922133
GSHP	1833	0.012533	0.549533	0.438133
GSHP	1892	0.0154	0.0414	0.943267
BORD	1648	0.1348	0.036733	0.8286
BORD	1828	0.017867	0.032733	0.949467
BORD	1829	0.006667	0.211667	0.781733
BORD	2002	0.026467	0.061533	0.911933
BORD	2003	0.044533	0.055467	0.9
BEDT	1422	0.009067	0.3274	0.6634
BEDT	1423	0.007933	0.189867	0.802333
BEDT	1424	0.017533	0.1126	0.870133
BEDT	1426	0.014933	0.238867	0.7462
CLSP	1008	0.01	0.7082	0.281667
CLSP	1009	0.005333	0.637667	0.3572
CLSP	1802	0.010467	0.666267	0.323267
CLSP	2312	0.005	0.752	0.242867
CLSP	2314	0.006067	0.7524	0.2416
IBIZ	1147	0.011533	0.1148	0.8738
IBIZ	1148	0.0164	0.235267	0.7482
IBIZ	1162	0.013	0.055133	0.932
IBIZ	1172	0.0232	0.1398	0.837
IBIZ	1280	0.022333	0.175667	0.801867
RHOD	1444	0.007267	0.143733	0.848733
RHOD	1454	0.027467	0.127333	0.845067
RHOD	1505	0.011	0.135467	0.853467
RHOD	1592	0.010067	0.5242	0.4658
RHOD	1609	0.008133	0.110267	0.881467
DACH	1051	0.0216	0.564	0.414467
DACH	1052	0.015267	0.618867	0.365733
DACH	1053	0.015533	0.563867	0.420667
DACH	1054	0.0254	0.728467	0.246133
DACH	1055	0.016667	0.6114	0.3718
AUSS	1336	0.17	0.2254	0.6046
AUSS	1337	0.016133	0.237267	0.7464
AUSS	1500	0.012067	0.026	0.962133
AUSS	1521	0.1014	0.3078	0.590867
AUSS	1683	0.0128	0.210267	0.776933
CHIH	1202	0.007267	0.219867	0.7728
CHIH	1203	0.022	0.0794	0.898667
CHIH	1204	0.014467	0.104733	0.880667
CHIH	1205	0.1532	0.3324	0.514333
CHIH	1206	0.0068	0.388867	0.6042
KERY	13878	0.007533	0.159533	0.833067
KERY	1483	0.0064	0.175733	0.817867
KERY	1579	0.012133	0.034067	0.953533
KERY	2014	0.004333	0.339933	0.655933
KERY	24255	0.009733	0.294667	0.695467
SCHP	1386	0.0092	0.0818	0.9088
SCHP	1471	0.013867	0.077267	0.908933
SCHP	1814	0.0104	0.090933	0.898667
SCHP	1852	0.013067	0.013733	0.973333
IRTR	2152	0.011533	0.1228	0.865533
IRTR	2189	0.0128	0.413133	0.5742
IRTR	2238	0.006667	0.4018	0.591467
IRTR	2242	0.009667	0.282267	0.7082
FCR	1188	0.0058	0.172933	0.821267
FCR	2020	0.006267	0.020467	0.973267
FCR	2042	0.006067	0.123533	0.870267
FCR	2044	0.006533	0.0468	0.946733
FCR	2259	0.004667	0.199467	0.796
SCWT	1624	0.081533	0.640867	0.2776
SCWT	1770	0.005933	0.3122	0.682
SCWT	2250	0.006867	0.422133	0.571
SCWT	2301	0.021667	0.636533	0.3418
POM	1190	0.155933	0.333533	0.5108
POM	1191	0.010667	0.731067	0.258267
POM	1210	0.050933	0.3128	0.636333
POM	1238	0.007867	0.163933	0.827933
POM	1239	0.203467	0.0754	0.721
LAB	1310	0.119267	0.587867	0.292733
LAB	1465	0.016267	0.392	0.591933
LAB	1468	0.022733	0.3696	0.6078
LAB	1754	0.0192	0.791933	0.188867
LAB	1830	0.006333	0.538667	0.454867
PRES	1082	0.009467	0.803133	0.187667
PRES	1096	0.0064	0.797133	0.1968
PRES	1115	0.012333	0.656733	0.330733
PRES	1127	0.0976	0.877933	0.024533
PRES	1095	0.083267	0.823733	0.0932
ROTT	1014	0.015867	0.725267	0.258933
ROTT	1028	0.006667	0.7466	0.246533
ROTT	1029	0.004867	0.9082	0.086867
ROTT	1033	0.007133	0.946867	0.045933
ROTT	1034	0.006467	0.921933	0.071733
BULM	1105	0.0064	0.954333	0.0392
BULM	1106	0.005667	0.552933	0.4414
BULM	1107	0.0256	0.9174	0.057267
BULM	1108	0.0084	0.9536	0.038
BULM	1109	0.0064	0.9706	0.023267
NEWF	271	0.0176	0.865867	0.116467
NEWF	274	0.006533	0.9628	0.030333
NEWF	275	0.006467	0.983733	0.009867
NEWF	277	0.0074	0.983867	0.008667
NEWF	278	0.086	0.862667	0.051467
GSD	1666	0.007	0.954733	0.038133
GSD	1776	0.003733	0.958067	0.0382
GSD	2011	0.009867	0.893933	0.096067
GSD	2060	0.0064	0.8242	0.169467
GSD	2086	0.006933	0.917267	0.075733
FBUL	1507	0.0122	0.975067	0.012933
FBUL	1508	0.0082	0.970733	0.0212
FBUL	1509	0.005	0.986333	0.008933
FBUL	2671	0.023467	0.918267	0.0582
MBLT	1915	0.007	0.936867	0.055933
MBLT	2253	0.008133	0.953533	0.038467
MBLT	2254	0.060133	0.904933	0.034933
MBLT	2255	0.010533	0.957533	0.031867
MBLT	2256	0.0066	0.985667	0.0078
BULD	1193	0.021133	0.964667	0.0142
BULD	1194	0.0056	0.9872	0.007067
BULD	1195	0.003933	0.988533	0.0074
BULD	1197	0.007133	0.9042	0.0888
BULD	1198	0.006733	0.9778	0.0154
BOX	1176	0.0038	0.982933	0.0132
BOX	1177	0.0044	0.9746	0.020933
BOX	1178	0.005733	0.9872	0.007133
BOX	1179	0.002933	0.9922	0.004733
BOX	1304	0.003733	0.9868	0.009667
MAST	1015	0.0052	0.943267	0.0516
MAST	1016	0.0114	0.9228	0.065867
MAST	1017	0.006133	0.913733	0.08
MAST	1066	0.0174	0.9588	0.023733
MAST	991	0.017933	0.965933	0.016067
BMD	941	0.004867	0.9596	0.035667
BMD	943	0.013133	0.7552	0.231733
BMD	968	0.010467	0.949133	0.040333
BMD	1763	0.005733	0.938867	0.055267
BMD	969	0.005067	0.902933	0.092067
GSMD	1547	0.007533	0.4592	0.533067
GSMD	1659	0.006133	0.687133	0.3066
GSMD	1660	0.017067	0.4854	0.4974
GSMD	1662	0.063933	0.632667	0.303133
GSMD	1663	0.009933	0.5714	2.93

TABLE 19C

Canid	Canid	k = 2, 15 Run Average	
Population^a	ID No.	Pop1	Pop2
SHIB	1769	0.9954	0.0046
SHIB	1854	0.991133	0.008867
SHIB	1856	0.9642	0.0358
SHIB	1860	0.992133	0.007867
SHIB	1981	0.989467	0.010533
CHOW	1633	0.993733	0.006267
CHOW	1835	0:994867	0.005133
CHOW	1837	0.991533	0.008467
CHOW	1838	0.995	0.005
CHOW	1839	0.988	0.012
AKIT	1130	0.9788	0.0212
AKIT	1131	0.995067	0.004933
AKIT	1132	0.995267	0.004733
AKIT	1133	0.994933	0.005067
AKIT	1134	0.996	0.004
AMAL	1629	0.8468	0.1532
AMAL	1779	0.816733	0.183267
AMAL	1845	0.913667	0.086333
AMAL	2132	0.934867	0.065133
AMAL	2214	0.9108	0.0892
BSJI	1338	0.735267	0.264733
BSJI	1339	0.986933	0.013067
BSJI	1645	0.989667	0.010333
BSJI	1675	0.9814	0.0186
BSJI	1717	0.984867	0.015133
SHAR	1573	0.9826	0.0174
SHAR	1593	0.932	0.068
SHAR	1619	0.931133	0.068867
SHAR	1998	0.7944	0.2056
SHAR	1999	0.9768	0.0232
HUSK	1469	0.916333	0.083667
HUSK	1883	0.939	0.061
HUSK	2115	0.797333	0.202667
HUSK	2117	0.642933	0.357067
HUSK	2118	0.889267	0.110733
AFGH	1812	0.582533	0.417467
AFGH	1939	0.6042	0.3958
AFGH	2264	0.572067	0.427933
AFGH	1936	0.7372	0.2628
AFGH	1937	0.666533	0.333467
SALU	1491	0.427467	0.572533
SALU	1535	0.6256	0.3744
SALU	1607	0.548533	0.451467
SALU	1873	0.323	0.677
SALU	2610	0.452133	0.547867
TIBT	1466	0.463867	0.536133
TIBT	1562	0.334267	0.665733
TIBT	1707	0.369133	0.630867
TIBT	26078	0.402067	0.597933
TIBT	28086	0.160333	0.839667
LHSA	1524	0.547533	0.452467
LHSA	1525	0.5422	0.4578
LHSA	1526	0.453533	0.546467
LHSA	1528	0.339	0.661
LHSA	2074	0.688267	0.311733
SAMO	1375	0.303933	0.696067
SAMO	1532	0.592467	0.407533
SAMO	1560	0.5672	0.4328
SAMO	169	0.461933	0.538067
SAMO	239	0.4442	0.5558
PEKE	1143	0.7292	0.2708
PEKE	1145	0.4824	0.5176
PEKE	1211	0.4778	0.5222
PEKE	1212	0.351067	0.648933
PEKE	1213	0.638467	0.361533
SHIH	1393	0.385467	0.614533
SHIH	1783	0.4202	0.5798
SHIH	2068	0.433667	0.566333
SHIH	2859	0.481267	0.518733
SHIH	2860	0.542	0.458
IWOF	1581	0.018867	0.981133
IWOF	1761	0.0092	0.9908
IWOF	1792	0.017467	0.982533
IWOF	1906	0.061533	0.938467
IWOF	1993	0.0062	0.9938

TABLE 19C-continued

Canid	Canid	k = 2, 15 Run Average	
Population^a	ID No.	Pop1	Pop2
STBD	1075	0.035	0.965
STBD	1714	0.056733	0.943267
STBD	1750	0.045267	0.954733
STBD	2403	0.019667	0.980333
STBD	2404	0.021467	0.978533
GREY	2477	0.155267	0.844733
GREY	2478	0.0156	0.9844
GREY	2479	0.0088	0.9912
GREY	2480	0.1108	0.8892
GREY	2481	0.0092	0.9908
BELS	1351	0.030333	0.969667
BELS	2111	0.1014	0.8986
BELS	2153	0.0072	0.9928
BELS	2209	0.053933	0.946067
BELS	2210	0.0352	0.9648
TURV	1622	0.0158	0.9842
TURV	2194	0.0078	0.9922
TURV	2200	0.030867	0.969133
TURV	2222	0.006133	0.993867
BORZ	1378	0.2322	0.7678
BORZ	1401	0.170933	0.829067
BORZ	1808	0.229267	0.770733
BORZ	2268	0.1112	0.8888
BORZ	978	0.102267	0.897733
COLL	1692	0.011133	0.988867
COLL	1701	0.0226	0.9774
COLL	2284	0.015333	0.984667
COLL	373	0.009267	0.990733
COLL	379	0.006133	0.993867
SSHP	1379	0.027867	0.972133
SSHP	1523	0.054133	0.945867
SSHP	1824	0.008133	0.991867
SSHP	1921	0.0048	0.9952
SSHP	2040	0.0838	0.9162
PUG	1077	0.028133	0.971867
PUG	1104	0.104933	0.895067
PUG	1183	0.159933	0.840067
PUG	1184	0.027533	0.972467
PUG	1192	0.009467	0.990533
KOMO	1484	0.025667	0.974333
KOMO	1964	0.0836	0.9164
KOMO	2321	0.035333	0.964667
KOMO	2323	0.091133	0.908867
KOMO	2334	0.0158	0.9842
WHIP	1355	0.0084	0.9916
WHIP	1395	0.008133	0.991867
WHIP	1407	0.005533	0.994467
WHIP	1409	0.006	0.994
WHIP	1518	0.005267	0.994733
SPOO	1530	0.044667	0.955333
SPOO	1582	0.050467	0.949533
SPOO	1876	0.022133	0.977867
SPOO	1877	0.011933	0.988067
SPOO	2337	0.0062	0.9938
BICH	1943	0.131	0.869
BICH	1954	0.286533	0.713467
BICH	933	0.056867	0.943133
BICH	974	0.142267	0.857733
KEES	1501	0.059533	0.940467
KEES	1589	0.009067	0.990933
KEES	1818	0.018533	0.981467
KEES	1819	0.007	0.993
KEES	2072	0.0066	0.9934
MNTY	1539	0.010933	0.989067
MNTY	1732	0.022533	0.977467
MNTY	2145	0.012533	0.987467
MNTY	2149	0.011333	0.988667
NELK	2216	0.107867	0.892133
NELK	2239	0.220267	0.779733
NELK	2240	0.037333	0.962667
NELK	2281	0.0152	0.9848
NELK	2295	0.2866	0.7134
KUVZ	1482	0.1712	0.8288
KUVZ	1551	0.2862	0.7138
KUVZ	1672	0.110333	0.889667

TABLE 19C-continued

Canid Population^a	Canid ID No.	k = 2, 15 Run Average	
		Pop1	Pop2
KUVZ	1913	0.041067	0.958933
KUVZ	1994	0.104667	0.895333
DANE	1574	0.018667	0.981333
DANE	1575	0.153333	0.846667
DANE	1580	0.0202	0.9798
DANE	1700	0.007333	0.992667
DANE	1748	0.1858	0.8142
WSSP	1955	0.006133	0.993867
WSSP	2139	0.015867	0.984133
WSSP	2143	0.005067	0.994933
WSSP	2195	0.020133	0.979867
WSSP	2286	0.005333	0.994667
DOBP	1031	0.014467	0.985533
DOBP	1032	0.062467	0.937533
DOBP	1749	0.052933	0.947067
DOBP	2162	0.0146	0.9854
DOBP	2245	0.0092	0.9908
SSNZ	13352	0.003467	0.996533
SSNZ	1360	0.003	0.997
SSNZ	1827	0.004867	0.995133
SSNZ	20457	0.010667	0.989333
SSNZ	22647	0.006267	0.993733
ITGY	1568	0.025333	0.974667
ITGY	1570	0.016533	0.983467
ITGY	1862	0.137667	0.862333
ITGY	1881	0.0804	0.9196
ITGY	1882	0.159933	0.840067
OES	1984	0.0414	0.9586
OES	2171	0.009067	0.990933
OES	2179	0.008133	0.991867
OES	1914	0.0212	0.9788
OES	2626	0.142733	0.857267
AMWS	2168	0.010867	0.989133
AMWS	2279	0.007733	0.992267
AMWS	2327	0.080333	0.919667
AMWS	987	0.014133	0.985867
AMWS	988	0.015467	0.984533
MSNZ	1587	0.005	0.995
MSNZ	1756	0.008267	0.991733
MSNZ	1851	0.004667	0.995333
MSNZ	2034	0.039	0.961
MSNZ	2613	0.004867	0.995133
AUST	1387	0.036867	0.963133
AUST	1531	0.009	0.991
AUST	1564	0.006133	0.993867
AUST	1870	0.051467	0.948533
AUST	1871	0.0066	0.9934
ECKR	1376	0.004133	0.995867
ECKR	1377	0.003933	0.996067
ECKR	1400	0.002933	0.997067
ECKR	1404	0.003133	0.996867
ECKR	1511	0.0066	0.9934
IRSE	1540	0.003267	0.996733
IRSE	1617	0.004133	0.995867
IRSE	1896	0.0136	0.9864
IRSE	2084	0.004533	0.995467
IRSE	2085	0.003533	0.996467
WHWT	1388	0.016133	0.983867
WHWT	1420	0.031467	0.968533
WHWT	1992	0.0064	0.9936
WHWT	2100	0.0078	0.9922
WHWT	2128	0.010867	0.989133
PNTR	1382	0.015	0.985
PNTR	1383	0.0574	0.9426
PNTR	1869	0.0322	0.9678
PNTR	1938	0.009867	0.990133
PNTR	1948	0.2778	0.7222
BASS	1341	0.024267	0.975733
BASS	1342	0.012733	0.987267
BASS	1506	0.006667	0.993333
BASS	1917	0.0066	0.9934
CKCS	1513	0.070867	0.929133
CKCS	1639	0.0084	0.9916
CKCS	1640	0.0086	0.9914
CKCS	1642	0.007267	0.992733

TABLE 19C-continued

Canid Population^a	Canid ID No.	k = 2, 15 Run Average	
		Pop1	Pop2
CKCS	2054	0.007067	0.992933
GSNZ	1868	0.274133	0.725867
GSNZ	22739	0.177133	0.822867
GSNZ	27093	0.087533	0.912467
GSNZ	27106	0.0126	0.9874
GSNZ	33390	0.008333	0.991667
PHAR	1292	0.1702	0.8298
PHAR	1947	0.275533	0.724467
PHAR	1962	0.1786	0.8214
PHAR	1963	0.158467	0.841533
GOLD	591	0.0048	0.9952
GOLD	592	0.029667	0.970333
GOLD	593	0.005933	0.994067
GOLD	603	0.007267	0.992733
GOLD	604	0.003333	0.996667
BEAG	1323	0.0084	0.9916
BEAG	1324	0.037133	0.962867
BEAG	1327	0.006667	0.993333
BEAG	994	0.0264	0.9736
BEAG	995	0.030333	0.969667
BLDH	1186	0.007733	0.992267
BLDH	1223	0.011667	0.988333
BLDH	1410	0.005267	0.994733
BLDH	1942	0.008933	0.991067
BLDH	1957	0.0058	0.9942
AIRT	1603	0.072867	0.927133
AIRT	1604	0.007	0.993
AIRT	1788	0.005667	0.994333
AIRT	1875	0.029867	0.970133
ACKR	1035	0.0096	0.9904
ACKR	2261	0.023267	0.976733
ACKR	2310	0.003667	0.996333
ACKR	1956	0.012333	0.987667
ACKR	2260	0.0052	0.9948
AHRT	1120	0.011133	0.988867
AHRT	1121	0.010067	0.989933
AHRT	1122	0.007533	0.992467
AHRT	1123	0.0102	0.9898
AHRT	1124	0.006467	0.993533
CHBR	1546	0.009667	0.990333
CHBR	1549	0.088867	0.911133
CHBR	1813	0.0042	0.9958
CHBR	2091	0.011	0.989
CHBR	888	0.004267	0.995733
CAIR	1405	0.009	0.991
CAIR	2096	0.029667	0.970333
CAIR	2113	0.0138	0.9862
CAIR	2125	0.006333	0.993667
CAIR	2131	0.020467	0.979533
PTWD	P142	0.005333	0.994667
PTWD	P1	0.0038	0.9962
PTWD	P238	0.011533	0.988467
PTWD	P25	0.0044	0.9956
PTWD	P67	0.006933	0.993067
GSHP	1628	0.004733	0.995267
GSHP	1708	0.048067	0.951933
GSHP	1710	0.040933	0.959067
GSHP	1833	0.007667	0.992333
GSHP	1892	0.008733	0.991267
BORD	1648	0.164267	0.835733
BORD	1828	0.0184	0.9816
BORD	1829	0.0054	0.9946
BORD	2002	0.033	0.967
BORD	2003	0.045267	0.954733
BEDT	1422	0.006933	0.993067
BEDT	1423	0.0062	0.9938
BEDT	1424	0.018133	0.981867
BEDT	1426	0.01	0.99
CLSP	1008	0.0074	0.9926
CLSP	1009	0.004067	0.995933
CLSP	1802	0.006667	0.993333
CLSP	2312	0.004133	0.995867
CLSP	2314	0.005067	0.994933
IBIZ	1147	0.011467	0.988533
IBIZ	1148	0.030933	0.969067

TABLE 19C-continued

Canid Population[a]	Canid ID No.	k = 2, 15 Run Average	
		Pop1	Pop2
IBIZ	1162	0.0162	0.9838
IBIZ	1172	0.017867	0.982133
IBIZ	1280	0.018733	0.981267
RHOD	1444	0.004333	0.995667
RHOD	1454	0.018	0.982
RHOD	1505	0.008	0.992
RHOD	1592	0.006733	0.993267
RHOD	1609	0.005067	0.994933
DACH	1051	0.0188	0.9812
DACH	1052	0.009067	0.990933
DACH	1053	0.016733	0.983267
DACH	1054	0.028867	0.971133
DACH	1055	0.009933	0.990067
AUSS	1336	0.1524	0.8476
AUSS	1337	0.013133	0.986867
AUSS	1500	0.010667	0.989333
AUSS	1521	0.102067	0.897933
AUSS	1683	0.008467	0.991533
CHIH	1202	0.005267	0.994733
CHIH	1203	0.03	0.97
CHIH	1204	0.013333	0.986667
CHIH	1205	0.166867	0.833133
CHIH	1206	0.004867	0.995133
KERY	13878	0.0066	0.9934
KERY	1483	0.005867	0.994133
KERY	1579	0.011133	0.988867
KERY	2014	0.0034	0.9966
KERY	24255	0.007267	0.992733
SCHP	1386	0.0082	0.9918
SCHP	1471	0.020933	0.979067
SCHP	1814	0.007667	0.992333
SCHP	1852	0.0184	0.9816
IRTR	2152	0.009333	0.990667
IRTR	2189	0.008333	0.991667
IRTR	2238	0.005467	0.994533
IRTR	2242	0.0076	0.9924
FCR	1188	0.004267	0.995733
FCR	2020	0.0052	0.9948
FCR	2042	0.004333	0.995667
FCR	2044	0.005133	0.994867
FCR	2259	0.003733	0.996267
SCWT	1624	0.051067	0.948933
SCWT	1770	0.004467	0.995533
SCWT	2250	0.005533	0.994467
SCWT	2301	0.0124	0.9876
POM	1190	0.181067	0.818933
POM	1191	0.006067	0.993933
POM	1210	0.049267	0.950733
POM	1238	0.010067	0.989933
POM	1239	0.298467	0.701533
LAB	1310	0.0756	0.9244
LAB	1465	0.011	0.989
LAB	1468	0.013533	0.986467
LAB	1754	0.007067	0.992933
LAB	1830	0.0052	0.9948
PRES	1082	0.009	0.991
PRES	1096	0.004667	0.995333
PRES	1115	0.008667	0.991333
PRES	1127	0.147867	0.852133
PRES	1095	0.115533	0.884467
ROTT	1014	0.016467	0.983533
ROTT	1028	0.005333	0.994667
ROTT	1029	0.003733	0.996267
ROTT	1033	0.006933	0.993067
ROTT	1034	0.003867	0.996133
BULM	1105	0.004067	0.995933
BULM	1106	0.004467	0.995533
BULM	1107	0.007933	0.992067
BULM	1108	0.005533	0.994467
BULM	1109	0.004533	0.995467
NEWF	271	0.014333	0.985667
NEWF	274	0.005867	0.994133
NEWF	275	0.006467	0.993533
NEWF	277	0.008933	0.991067
NEWF	278	0.106	0.894
GSD	1666	0.005467	0.994533
GSD	1776	0.003	0.997
GSD	2011	0.004267	0.995733
GSD	2060	0.004467	0.995533
GSD	2086	0.005867	0.994133
FBUL	1507	0.016867	0.983133
FBUL	1508	0.0084	0.9916
FBUL	1509	0.0066	0.9934
FBUL	2671	0.032867	0.967133
MBLT	1915	0.005467	0.994533
MBLT	2253	0.007467	0.992533
MBLT	2254	0.063667	0.936333
MBLT	2255	0.006333	0.993667
MBLT	2256	0.0102	0.9898
BULD	1193	0.035	0.965
BULD	1194	0.010067	0.989933
BULD	1195	0.010867	0.989133
BULD	1197	0.0042	0.9958
BULD	1198	0.005133	0.994867
BOX	1176	0.003133	0.996867
BOX	1177	0.003467	0.996533
BOX	1178	0.005533	0.994467
BOX	1179	0.004467	0.995533
BOX	1304	0.0046	0.9954
MAST	1015	0.003533	0.996467
MAST	1016	0.012467	0.987533
MAST	1017	0.006933	0.993067
MAST	1066	0.011333	0.988667
MAST	991	0.0132	0.9868
BMD	941	0.0054	0.9946
BMD	943	0.0054	0.9946
BMD	968	0.005933	0.994067
BMD	1763	0.004133	0.995867
BMD	969	0.0034	0.9966
GSMD	1547	0.004867	0.995133
GSMD	1659	0.004467	0.995533
GSMD	1660	0.010933	0.989067
GSMD	1662	0.0276	0.9724
GSMD	1663	0.009267	0.990733

[a]See Table 5 for abbreviations of canid populations.

KBB: pbe

TABLE 19D

Canid Population[a]	Canid ID No.	k = 2 with wolf, 15 Run Average	
		Pop1	Pop2
WOLF	W511	0.994	0.006
WOLF	W5131	0.982	0.018
WOLF	WC3	0.995	0.005
WOLF	WE10	0.995	0.005
WOLF	282135	0.9918	0.0082
WOLF	492-8	0.9968	0.0032
WOLF	930121	0.9858	0.0142
WOLF	Iran-1	0.9388	0.0612
SHIB	1769	0.993	0.007
SHIB	1854	0.98	0.02
SHIB	1856	0.938	0.062
SHIB	1860	0.99	0.01
SHIB	1981	0.987	0.013
CHOW	1633	0.9904	0.0096
CHOW	1835	0.9916	0.0084
CHOW	1837	0.9774	0.0226
CHOW	1838	0.9918	0.0082
CHOW	1839	0.9796	0.0204
AKIT	1130	0.9724	0.0276
AKIT	1131	0.993	0.007
AKIT	1132	0.9934	0.0066
AKIT	1133	0.995	0.005
AKIT	1134	0.994	0.006
AMAL	1629	0.5876	0.4124

TABLE 19D-continued

Canid	Canid	k = 2 with wolf, 15 Run Average	
Population^a	ID No.	Pop1	Pop2
AMAL	1779	0.516	0.484
AMAL	1845	0.6802	0.3198
AMAL	2132	0.755	0.245
AMAL	2214	0.7298	0.2702
BSJI	1338	0.7944	0.2056
BSJI	1339	0.976	0.024
BSJI	1645	0.9792	0.0208
BSJI	1675	0.9718	0.0282
BSJI	1717	0.9672	0.0328
SHAR	1573	0.9318	0.0682
SHAR	1593	0.914	0.086
SHAR	1619	0.8048	0.1952
SHAR	1998	0.6918	0.3082
SHAR	1999	0.9372	0.0628
HUSK	1469	0.702	0.298
HUSK	1883	0.7878	0.2122
HUSK	2115	0.5934	0.4066
HUSK	2117	0.5412	0.4588
HUSK	2118	0.7718	02282
AFGH	1812	0.4642	0.5358
AFGH	1939	0.5172	0.4828
AFGH	2264	0.4348	0.5652
AFGH	1936	0.5942	0.4058
AFGH	1937	0.583	0.417
SALU	1491	0.3624	0.6376
SALU	1535	0.4792	0.5208
SALU	1607	0.4234	0.5766
SALU	1873	0.2304	0.7696
SALU	2610	0.4092	0.5908
TIBT	1466	0.3684	0.6316
TIBT	1562	0.2896	0.7104
TIBT	1707	0.3136	0.6864
TIBT	26078	0.3314	0.6686
TIBT	28086	0.1316	0.8684
LHSA	1524	0.4598	0.5402
LHSA	1525	0.4652	0.5348
LHSA	1526	0.4	0.6
LHSA	1528	0.2798	0.7202
LHSA	2074	0.5838	0.4162
SAMO	1375	0.1684	0.8316
SAMO	1532	0.5154	0.4846
SAMO	1560	0.4444	0.5556
SAMO	169	0.3686	0.6314
SAMO	239	0.3666	0.6334
PEKE	1143	0.5856	0.4144
PEKE	1145	0.3948	0.6052
PEKE	1211	0.416	0.584
PEKE	1212	0.2806	0.7194
PEKE	1213	0.4832	0.5168
SHIH	1393	0.3196	0.6804
SHIH	1783	0.3234	0.6766
SHIH	2068	0.347	0.653
SHIH	2859	0.3476	0.6524
SHIH	2860	0.4582	0.5418
IWOF	1581	0.0124	0.9876
IWOF	1761	0.0054	0.9946
IWOF	1792	0.0086	0.9914
IWOF	1906	0.026	0.974
IWOF	1993	0.0046	0.9954
STBD	1075	0.0348	0.9652
STBD	1714	0.0484	0.9516
STBD	1750	0.028	0.972
STBD	2403	0.021	0.979
STBD	2404	0.0122	0.9878
GREY	2477	0.0992	0.9008
GREY	2478	0.0146	0.9854
GREY	2479	0.0062	0.9938
GREY	2480	0.1026	0.8974
GREY	2481	0.0058	0.9942
BELS	1351	0.0142	0.9858
BELS	2111	0.0206	0.9794
BELS	2153	0.0058	0.9942
BELS	2209	0.036	0.964
BELS	2210	0.0268	0.9732
TURV	1622	0.0184	0.9816

TABLE 19D-continued

Canid	Canid	k = 2 with wolf, 15 Run Average	
Population^a	ID No.	Pop1	Pop2
TURV	2194	0.0062	0.9938
TURV	2200	0.0178	0.9822
TURV	2222	0.0058	0.9942
BORZ	1378	0.1582	0.8418
BORZ	1401	0.1348	0.8652
BORZ	1808	0.1496	0.8504
BORZ	2268	0.0448	0.9552
BORZ	978	0.0282	0.9718
COLL	1692	0.0102	0.9898
COLL	1701	0.0236	0.9764
COLL	2284	0.0178	0.9822
COLL	373	0.0102	0.9898
COLL	379	0.0064	0.9936
SSHP	1379	0.0186	0.9814
SSHP	1523	0.055	0.945
SSHP	1824	0.0058	0.9942
SSHP	1921	0.0048	0.9952
SSHP	2040	0.0678	0.9322
PUG	1077	0.014	0.986
PUG	1104	0.0376	0.9624
PUG	1183	0.1068	0.8932
PUG	1184	0.0102	0.9898
PUG	1192	0.0064	0.9936
KOMO	1484	0.0138	0.9862
KOMO	1964	0.1264	0.8736
KOMO	2321	0.0356	0.9644
KOMO	2323	0.072	0.928
KOMO	2334	0.0368	0.9632
WHIP	1355	0.005	0.995
WHIP	1395	0.006	0.994
WHIP	1407	0.0048	0.9952
WHIP	1409	0.0034	0.9966
WHIP	1518	0.0038	0.9962
SPOO	1530	0.0322	0.9678
SPOO	1582	0.033	0.967
SPOO	1876	0.0276	0.9724
SPOO	1877	0.0108	0.9892
SPOO	2337	0.0038	0.9962
BICH	1943	0.0252	0.9748
BICH	1954	0.2126	0.7874
BICH	933	0.0202	0.9798
BICH	974	0.09	0.91
KEES	1501	0.0352	0.9648
KEES	1589	0.012	0.988
KEES	1818	0.0182	0.9818
KEES	1819	0.005	0.995
KEES	2072	0.0054	0.9946
MNTY	1539	0.0104	0.9896
MNTY	1732	0.013	0.987
MNTY	2145	0.0126	0.9874
MNTY	2149	0.0068	0.9932
NELK	2216	0.0596	0.9404
NELK	2239	0.1338	0.8662
NELK	2240	0.0184	0.9816
NELK	2281	0.0078	0.9922
NELK	2295	0.1786	0.8214
KUVZ	1482	0.0726	0.9274
KUVZ	1551	0.2054	0.7946
KUVZ	1672	0.0846	0.9154
KUVZ	1913	0.012	0.988
KUVZ	1994	0.0654	0.9346
DANE	1574	0.0118	0.9882
DANE	1575	0.1232	0.8768
DANE	1580	0.0138	0.9862
DANE	1700	0.0046	0.9954
DANE	1748	0.0798	0.9202
WSSP	1955	0.004	0.996
WSSP	2139	0.0132	0.9868
WSSP	2143	0.0068	0.9932
WSSP	2195	0.0724	0.9276
WSSP	2286	0.0038	0.9962
DOBP	1031	0.0126	0.9874
DOBP	1032	0.1052	0.8948
DOBP	1749	0.0692	0.9308
DOBP	2162	0.0136	0.9864

TABLE 19D-continued

Canid Population[a]	Canid ID No.	k = 2 with wolf, 15 Run Average	
		Pop1	Pop2
DOBP	2245	0.0104	0.9896
SSNZ	13352	0.003	0.997
SSNZ	1360	0.0024	0.9976
SSNZ	1827	0.004	0.996
SSNZ	20457	0.0118	0.9882
SSNZ	22647	0.0048	0.9952
ITGY	1568	0.0098	0.9902
ITGY	1570	0.0132	0.9868
ITGY	1862	0.0478	0.9522
ITGY	1881	0.0746	0.9254
ITGY	1882	0.1056	0.8944
OES	1984	0.0508	0.9492
OES	2171	0.0068	0.9932
OES	2179	0.005	0.995
OES	1914	0.0148	0.9852
OES	2626	0.129	0.871
AMWS	2168	0.0194	0.9806
AMWS	2279	0.0062	0.9938
AMWS	2327	0.036	0.964
AMWS	987	0.0054	0.9946
AMWS	988	0.0116	0.9884
MSNZ	1587	0.004	0.996
MSNZ	1756	0.0076	0.9924
MSNZ	1851	0.0046	0.9954
MSNZ	2034	0.0374	0.9626
MSNZ	2613	0.0038	0.9962
AUST	1387	0.0208	0.9792
AUST	1531	0.0048	0.9952
AUST	1564	0.0038	0.9962
AUST	1870	0.026	0.974
AUST	1871	0.0038	0.9962
ECKR	1376	0.0056	0.9944
ECKR	1377	0.003	0.997
ECKR	1400	0.002	0.998
ECKR	1404	0.003	0.997
ECKR	1511	0.0048	0.9952
IRSE	1540	0.003	0.997
IRSE	1617	0.004	0.996
IRSE	1896	0.0104	0.9896
IRSE	2084	0.0046	0.9954
IRSE	2085	0.005	0.995
WHWT	1388	0.0084	0.9916
WHWT	1420	0.0328	0.9672
WHWT	1992	0.0058	0.9942
WHWT	2100	0.0054	0.9946
WHWT	2128	0.0074	0.9926
PNTR	1382	0.0368	0.9632
PNTR	1383	0.0748	0.9252
PNTR	1869	0.0274	0.9726
PNTR	1938	0.0166	0.9834
PNTR	1948	0.3046	0.6954
BASS	1341	0.0212	0.9788
BASS	1342	0.0078	0.9922
BASS	1506	0.005	0.995
BASS	1917	0.004	0.996
CKCS	1513	0.0502	0.9498
CKCS	1639	0.0058	0.9942
CKCS	1640	0.0068	0.9932
CKCS	1642	0.0074	0.9926
CKCS	2054	0.0064	0.9936
GSNZ	1868	0.224	0.776
GSNZ	22739	0.116	0.884
GSNZ	27093	0.0496	0.9504
GSNZ	27106	0.0094	0.9906
GSNZ	33390	0.0048	0.9952
PHAR	1292	0.1686	0.8314
PHAR	1947	0.3092	0.6908
PHAR	1962	0.1454	0.8546
PHAR	1963	0.0938	0.9062
GOLD	591	0.0058	0.9942
GOLD	592	0.0854	0.9146
GOLD	593	0.0072	0.9928
GOLD	603	0.0092	0.9908
GOLD	604	0.003	0.997
BEAG	1323	0.0048	0.9952
BEAG	1324	0.0458	0.9542
BEAG	1327	0.0068	0.9932
BEAG	994	0.0198	0.9802
BEAG	995	0.012	0.988
BLDH	1186	0.005	0.995
BLDH	1223	0.0086	0.9914
BLDH	1410	0.0038	0.9962
BLDH	1942	0.0068	0.9932
BLDH	1957	0.004	0.996
AIRT	1603	0.0658	0.9342
AIRT	1604	0.0052	0.9948
AIRT	1788	0.0046	0.9954
AIRT	1875	0.0272	0.9728
ACKR	1035	0.0066	0.9934
ACKR	2261	0.0326	0.9674
ACKR	2310	0.003	0.997
ACKR	1956	0.0108	0.9892
ACKR	2260	0.0038	0.9962
AHRT	1120	0.0084	0.9916
AHRT	1121	0.0068	0.9932
AHRT	1122	0.0054	0.9946
AHRT	1123	0.0104	0.9896
AHRT	1124	0.0058	0.9942
CHBR	1546	0.0058	0.9942
CHBR	1549	0.0746	0.9254
CHBR	1813	0.003	0.997
CHBR	2091	0.0178	0.9822
CHBR	888	0.0038	0.9962
CAIR	1405	0.0106	0.9894
CAIR	2096	0.0402	0.9598
CAIR	2113	0.0078	0.9922
CAIR	2125	0.0044	0.9956
CAIR	2131	0.0132	0.9868
PTWD	P142	0.0052	0.9948
PTWD	P1	0.0036	0.9964
PTWD	P238	0.0082	0.9918
PTWD	P25	0.004	0.996
PTWD	P67	0.0062	0.9938
GSHP	1628	0.0038	0.9962
GSHP	1708	0.0518	0.9482
GSHP	1710	0.0456	0.9544
GSHP	1833	0.0068	0.9932
GSHP	1892	0.0058	0.9942
BORD	1648	0.0938	0.9062
BORD	1828	0.0114	0.9886
BORD	1829	0.0034	0.9966
BORD	2002	0.0156	0.9844
BORD	2003	0.0452	0.9548
BEDT	1422	0.0048	0.9952
BEDT	1423	0.005	0.995
BEDT	1424	0.0302	0.9698
BEDT	1426	0.0072	0.9928
CLSP	1008	0.007	0.993
CLSP	1009	0.0042	0.9958
CLSP	1802	0.006	0.994
CLSP	2312	0.0038	0.9962
CLSP	2314	0.005	0.995
IBIZ	1147	0.011	0.989
IBIZ	1148	0.0974	0.9026
IBIZ	1162	0.0106	0.9894
IBIZ	1172	0.011	0.989
IBIZ	1280	0.0148	0.9852
RHOD	1444	0.0042	0.9958
RHOD	1454	0.0154	0.9846
RHOD	1505	0.006	0.994
RHOD	1592	0.0082	0.9918
RHOD	1609	0.0098	0.9902
DACH	1051	0.0166	0.9834
DACH	1052	0.0124	0.9876
DACH	1053	0.0178	0.9822
DACH	1054	0.051	0.949
DACH	1055	0.0072	0.9928
AUSS	1336	0.093	0.907
AUSS	1337	0.0182	0.9818
AUSS	1500	0.0206	0.9794

TABLE 19D-continued

Canid	Canid	k = 2 with wolf, 15 Run Average	
Population[a]	ID No.	Pop1	Pop2
AUSS	1521	0.0788	0.9212
AUSS	1683	0.0088	0.9912
CHIH	1202	0.004	0.996
CHIH	1203	0.0298	0.9702
CHIH	1204	0.0142	0.9858
CHIH	1205	0.1506	0.8494
CHIH	1206	0.004	0.996
KERY	13878	0.0054	0.9946
KERY	1483	0.0048	0.9952
KERY	1579	0.0058	0.9942
KERY	2014	0.0028	0.9972
KERY	24255	0.0052	0.9948
SCHP	1386	0.0136	0.9864
SCHP	1471	0.0646	0.9354
SCHP	1814	0.0076	0.9924
SCHP	1852	0.0162	0.9838
IRTR	2152	0.0086	0.9914
IRTR	2189	0.0048	0.9952
IRTR	2238	0.0048	0.9952
IRTR	2242	0.0066	0.9934
FCR	1188	0.004	0.996
FCR	2020	0.004	0.996
FCR	2042	0.004	0.996
FCR	2044	0.0038	0.9962
FCR	2259	0.0028	0.9972
SCWT	1624	0.035	0.965
SCWT	1770	0.0038	0.9962
SCWT	2250	0.004	0.996
SCWT	2301	0.0084	0.9916
POM	1190	0.1668	0.8332
POM	1191	0.0042	0.9958
POM	1210	0.0374	0.9626
POM	1238	0.0078	0.9922
POM	1239	0.3112	0.6888
LAB	1310	0.063	0.937
LAB	1465	0.0172	0.9828
LAB	1468	0.0124	0.9876
LAB	1754	0.006	0.994
LAB	1830	0.0076	0.9924
PRES	1082	0.0108	0.9892
PRES	1096	0.0052	0.9948
PRES	1115	0.0092	0.9908
PRES	1127	0.1526	0.8474
PRES	1095	0.0906	0.9094
ROTT	1014	0.0124	0.9876
ROTT	1028	0.0068	0.9932
ROTT	1029	0.0038	0.9962
ROTT	1033	0.0204	0.9796
ROTT	1034	0.0038	0.9962
BULM	1105	0.003	0.997
BULM	1106	0.0034	0.9966
BULM	1107	0.0082	0.9918
BULM	1108	0.005	0.995
BULM	1109	0.0066	0.9934
NEWF	271	0.0114	0.9886
NEWF	274	0.0052	0.9948
NEWF	275	0.0048	0.9952
NEWF	277	0.0078	0.9922
NEWF	278	0.1024	0.8976
GSD	1666	0.0058	0.9942
GSD	1776	0.003	0.997
GSD	2011	0.004	0.996
GSD	2060	0.0042	0.9958
GSD	2086	0.0046	0.9954
FBUL	1507	0.0098	0.9902
FBUL	1508	0.0058	0.9942
FBUL	1509	0.005	0.995
FBUL	2671	0.0464	0.9536
MBLT	1915	0.0038	0.9962
MBLT	2253	0.0054	0.9946
MBLT	2254	0.0454	0.9546
MBLT	2255	0.0046	0.9954
MBLT	2256	0.0078	0.9922
BULD	1193	0.0234	0.9766
BULD	1194	0.0098	0.9902
BULD	1195	0.0162	0.9838
BULD	1197	0.0042	0.9958
BULD	1198	0.0038	0.9962
BOX	1176	0.003	0.997
BOX	1177	0.003	0.997
BOX	1178	0.0048	0.9952
BOX	1179	0.004	0.996
BOX	1304	0.0058	0.9942
MAST	1015	0.0038	0.9962
MAST	1016	0.0104	0.9896
MAST	1017	0.0096	0.9904
MAST	1066	0.0078	0.9922
MAST	991	0.012	0.988
BMD	941	0.0056	0.9944
BMD	943	0.004	0.996
BMD	968	0.0058	0.9942
BMD	1763	0.003	0.997
BMD	969	0.0028	0.9972
GSMD	1547	0.004	0.996
GSMD	1659	0.003	0.997
GSMD	1660	0.006	0.994
GSMD	1662	0.0204	0.9796
GSMD	1663	0.0072	0.9928

[a]See Table 5 for abbreviations of canid populations.

KBB: pbe

TABLE 21A

	AHRT Canid ID NO (missing genotypes)			BASS Canid ID NO (missing genotypes)			BEAG Canid ID NO (missing genotypes)					
Canid population*	1119 (8)	1081 (2)	1121 (6)	24039 (19)	930 (3)	931 (3)	18586 (51)	18424 (13)	1323 (20)	1324 (16)	1325 (8)	1327 (12)
AHTR	0.19003	0	0.2457	0	0	0	3.00E−05	0	0	0	0	0
AMWS	0.00042	0	0	0	0	0	0	0	0	0	0	0
BASS	0	0	0	2.00E−05	2.00E−05	0.36647	0	0	0	0	0	0
BEAG	0	0	0	0	0	0.00068	0.00859	0.00634	0.99969	0.99504	0.99062	0.99804
BEAC	0	0	0	0	0	0.00014	0	0	0	0	0	0
BMD	0	0	0	0	0	0	1.00E−05	0	0	0.0049	0.00893	0
BICH	0	0	0	0	0	0	0	0	0	2.00E−05	0	0
BORZ	0	0	0	9.00E−05	0.00021	0	0.00012	0.01475	0	0	0	0
BOX	0	0	0	0	0	0	0	0	0	0	0	0
BULM	0	0.00023	0	0	1.00E−05	0.58998	0.00739	0	0	0	0	0
ACKR	0.0015	0	0	0	0	0	0	0	0	0	0	0
DACH	0.00304	0.99974	0.0102	0.99988	0.9996	0.03153	0.01324	0.97888	0	0	0	0.00142

TABLE 21A-continued

	AHRT Canid ID NO (missing genotypes)			BASS Canid ID NO (missing genotypes)			BEAG Canid ID NO (missing genotypes)					
Canid population*	1119 (8)	1081 (2)	1121 (6)	24039 (19)	930 (3)	931 (3)	18586 (51)	18424 (13)	1323 (20)	1324 (16)	1325 (8)	1327 (12)
DALM	0	0	0	0	0	0	0	0	0	0	0	0
ESPR	0	0	0.00011	0	0	0	0	0	0	0	0	0
FSP	0	0	0	0	0	0	0	0	0	0	0	0
FCR	0	0	0.2676	0	0	0	0.00017	0	0	0	0	0.00023
EFOX	0	0	0	0	0	0	7.00E−05	0	0	0	0	0
FBLD	0	0	0	0	0	0	0	0	0	0	0	0
GPIN	0	0	0.00039	0	0	0	0	0	0	0	0	0
GSHP	0.00029	0	0.00037	0	0	0	0	0	0	0	0	0
GOLD	0	1.00E−05	0.4753	0	0	0.00759	7.00E−05	0	0	0	0	0
IBIZ	0.76932	0	0.00027	0	0	0	0	0	0	0	0	0
IRSE	0	0	0	0	0	0	0	0	0	0	0	0
IRWS	0	0	0	0	0	0	0.001	0	0	0	0	0
LAB	0	0	0	0	0.00013	6.00E−05	0	0	0	0	0	0
MAST	0	0	0	0	0	0	0.92848	0	0	0	0	0
PBGV	0	0	0	0	0	0	2.00E−05	0	0	0	0	0
PAPI	0	0	0	0	0	0	3.00E−05	0	0	0	0	0
PTWD	0	0	0	0	0	0.00346	0	0	0	0	0	0
ROTT	0	0	0	0	0	0	0.04067	0	0.00029	0	0.00043	0
STBD	0.03485	0	0	0	0	0	0	0	0	0	0	0
SCDH	0	0	0	0	0	0	1.00E−05	0	0	0	0	0
SPIN	0	0	0	0	0	0	0	0	0	0	0	1.00E−05
SCOL	0	0	0	0	0	0	0	0	0	0	0	0
SSCH	0	0	0	0	0	0	0	1.00E−05	0	0	0	0.00028
WSSP	0.0005	0	0	0	0	1.00E−05	0	0	0	0	0	0

TABLE 21B

	BMD Canid Identification Number (missing genotypes)										Borzoi		
Canid population*	918 (16)	883 (6)	941 (7)	943 (11)	21287 (16)	968 (45)	970 (17)	971 (7)	973 (28)	976 (9)	1655 (24)	978 (0)	979 (22)
AHTR	0	0	0	0	0	0	0	0	0	0	0	0	0
AMWS	0	0	0	0	0	0	0	0	0	0	0	0	0
BASS	0	0	0	0	0	0	0	0	0	0	0	0.8529	0.00981
BEAG	0	0	0	0	0	0	0	0	0	0	0	0.00886	0
BEAC	0	0	0	0	0	0	0	0	0	0	0	0	0
BMD	0.99999	0.99999	0.99999	0.99995	0.99999	0.99999	0.99999	0.99999	0.99999	0.99999	0	0	0
BICH	0	0	0	0	0	0	0	0	0	0	0	0	0
BORZ	0	0	0	0	0	0	0	0	0	0	0	0.06219	0
BOX	0	0	0	0	0	0	0	0	0	0	0	0	0
BULM	0	0	0	0	0	0	0	0	0	0	0	0	0.0025
ACKR	0	0	0	0	0	0	0	0	0	0	0	0	0
DACH	0	0	0	0	0	0	0	0	0	0	0.99999	0.07511	0.98767
DALM	0	0	0	0	0	0	0	0	0	0	0	1.00E−05	0
ESPR	0	0	0	0	0	0	0	0	0	0	0	0	0
FSP	0	0	0	0	0	0	0	0	0	0	0	0	0
FCR	0	0	0	0	0	0	0	0	0	0	0	0	0
EFOX	0	0	0	0	0	0	0	0	0	0	0	4.00E−05	0
FBLD	0	0	0	0	0	0	0	0	0	0	0	0	0
GPIN	0	0	0	0	0	0	0	0	0	0	0	0	0
GSHP	0	0	0	0	0	0	0	0	0	0	0	0	0
GOLD	0	0	0	4.00E−05	0	0	0	0	0	0	0	0.0001	0
IBIZ	0	0	0	0	0	0	0	0	0	0	0	0	0
IRSE	0	0	0	0	0	0	0	0	0	0	0	0	0
IRWS	0	0	0	0	0	0	0	0	0	0	0	0	0
LAB	0	0	0	0	0	0	0	0	0	0	0	0.00018	0
MAST	0	0	0	0	0	0	0	0	0	0	0	4.00E−05	0
PBGV	0	0	0	0	0	0	0	0	0	0	0	0	0
PAPI	0	0	0	0	0	0	0	0	0	0	0	0.0005	0
PTWD	0	0	0	0	0	0	0	0	0	0	0	0	0
ROTT	0	0	0	0	0	0	0	0	0	0	0	0	0
STBD	0	0	0	0	0	0	0	0	0	0	0	0	0
SCDH	0	0	0	0	0	0	0	0	0	0	0	1.00E−05	0
SPIN	0	0	0	0	0	0	0	0	0	0	0	0	0
SCOL	0	0	0	0	0	0	0	0	0	0	0	0	0
SSCH	0	0	0	0	0	0	0	0	0	0	0	0	0
WSSP	0	0	0	0	0	0	0	0	0	0	0	0	0

TABLE 21C

	BOX Canid Identification Number (missing genotypes)										
Canid population*	584 (56)	585 (18)	583 (14)	586 (13)	587 (43)	588 (0)	589 (6)	590 (0)	997 (0)	1302 (30)	1304 (12)
AHTR	0	0	0	0	0	0	0	0	0	0	0
AMWS	0	0	0	0	0	0	0	0	0	0	0
BASS	0	0	0	0	0	0	0	0	0	0	0
BEAG	0	0	0	0	0	0	0	0	0	0	0
BEAC	0	0	0	0	0	0	0	0	0	0	0
BMD	0	0	0	0	0	0	0	0	0	0	0
BICH	0	0	0	0	0	0	0	0	0	0	0
BORZ	0	0	0	0	0	0	0	0	0	0	0
BOX	0.99999	0.99999	0.99999	0.99996	0.99996	0.99999	0.99391	0.99999	0.99999	0.99999	0.99999
BULM	0	0	0	0	0	0	0	0	0	0	0
ACKR	0	0	0	0	0	0	0	0	0	0	0
DACH	0	0	0	0	0	0	0.00153	0	0	0	0
DALM	0	0	0	0	0	0	0	0	0	0	0
ESPR	0	0	0	0	0	0	0	0	0	0	0
FSP	0	0	0	0	0	0	0	0	0	0	0
FCR	0	0	0	0	0	0	0	0	0	0	0
EFOX	0	0	0	0	0	0	0	0	0	0	0
FBLD	0	0	0	0	0	0	0	0	0	0	0
GPIN	0	0	0	0	0	0	0	0	0	0	0
GSHP	0	0	0	0	0	0	0	0	0	0	0
GOLD	0	0	0	3.00E−05	0	0	2.00E−05	0	0	0	0
IBIZ	0	0	0	0	0	0	0	0	0	0	0
IRSE	0	0	0	0	0	0	0	0	0	0	0
IRWS	0	0	0	0	0	0	0	0	0	0	0
LAB	0	0	0	0	0	0	0	0	0	0	0
MAST	0	0	0	0	0	0	0	0	0	0	0
PBGV	0	0	0	0	0	0	0	0	0	0	0
PAPI	0	0	0	0	0	0	0	0	0	0	0
PTWD	0	0	0	0	0	0	0	0	0	0	0
ROTT	0	0	0	0	3.00E−05	0	0.00451	0	0	0	0
STBD	0	0	0	0	0	0	0	0	0	0	0
SCDH	0	0	0	0	0	0	0	0	0	0	0
SPIN	0	0	0	0	0	0	0	0	0	0	0
SCOL	0	0	0	0	0	0	0	0	0	0	0
SSCH	0	0	0	0	0	0	0	0	0	0	0
WSSP	0	0	0	0	0	0	0	0	0	0	0

TABLE 21D

	BULM Canid Identification Number (missing genotypes)								FCR Canid Identification Number (missing genotypes)				
Canid population*	1098 (23)	1105 (4)	1106 (16)	1108 (24)	1109 (0)	1110 (5)	1111 (2)	1112 (11)	22417 (29)	746 (39)	752 (13)	839 (33)	791 (7)
AHTR	0	0	0	0	0	0	0	0	0	0	0	0	0
AMWS	0	0	0	0	0	0	0	0	0	0	0	0	0
BASS	0	0	0	0	0	0	0	0	0	0	0	0	0
BEAG	0	0	0	0	0	0	0	0	0	0	0	0	0
BEAC	0	0	0	0	0	0	0	0	0	0	0	0	0
BMD	0	0	0	0	0	0	0	0	0	0	0	0	0
BICH	0	0	0	0	0	0	0	0	0	0	0	0	0
BORZ	0	0	0	0	0	0	0	0	0	0	0	0	0
BOX	0	0	0	0	0	0	0	0	0	0	0	0	0
BULM	0.99999	0.99999	0.99998	0.99999	0.99999	0.99999	0.99999	0.99999	0	0	0	0	0
ACKR	0	0	0	0	0	0	0	0	0	0	0	0	0
DACH	0	0	0	0	0	0	0	0	0	0	0	0.00017	9.00E−05
DALM	0	0	0	0	0	0	0	0	0	0	0	0	0
ESPR	0	0	0	0	0	0	0	0	0	0	0	0	0
FSP	0	0	0	0	0	0	0	0	0	0	0	0	0
FCR	0	0	0	0	0	0	0	0	0.99999	0.99999	0	0.99982	0.99986
EFOX	0	0	0	0	0	0	0	0	0	0	0	0	0
FBLD	0	0	0	0	0	0	0	0	0	0	0	0	0
GPIN	0	0	0	0	0	0	0	0	0	0	0	0	0
GSHP	0	0	0	0	0	0	0	0	0	0	0	0	0
GOLD	0	0	1.00E−05	0	0	0	0	0	0	0	0.99997	0	0
IBIZ	0	0	0	0	0	0	0	0	0	0	0	0	0
IRSE	0	0	0	0	0	0	0	0	0	0	0	0	0
IRWS	0	0	0	0	0	0	0	0	0	0	0	0	0
LAB	0	0	0	0	0	0	0	0	0	0	0	0	0

TABLE 21D-continued

Canid population*	BULM Canid Identification Number (missing genotypes) 1098 (23)	1105 (4)	1106 (16)	1108 (24)	1109 (0)	1110 (5)	1111 (2)	1112 (11)	FCR Canid Identification Number (missing genotypes) 22417 (29)	746 (39)	752 (13)	839 (33)	791 (7)
MAST	0	0	0	0	0	0	0	0	0	0	0	0	0
PBGV	0	0	0	0	0	0	0	0	0	0	0	0	0
PAPI	0	0	0	0	0	0	0	0	0	0	0	0	0
PTWD	0	0	0	0	0	0	0	0	0	0	0	0	0
ROTT	0	0	0	0	0	0	0	0	0	0	2.00E−05	0	4.00E−05
STBD	0	0	0	0	0	0	0	0	0	0	0	0	0
SCDH	0	0	0	0	0	0	0	0	0	0	0	0	0
SPIN	0	0	0	0	0	0	0	0	0	0	0	0	0
SCOL	0	0	0	0	0	0	0	0	0	0	0	0	0
SSCH	0	0	0	0	0	0	0	0	0	0	0	0	0
WSSP	0	0	0	0	0	0	0	0	0	0	0	0	0

TABLE 21E

Canid population*	DACH Canid Identification Number (missing genotypes) 20345 (8)	20274 (14)	1036 (19)	1037 (9)	1038 (26)	1048 (15)	1049 (10)	1050 (8)	1060 (13)	1061 (28)
AHTR	0	0	0	0	0	0	0	0	0	0
AMWS	0	0	0	0	0	0	0	0	0	0
BASS	0	0	0	5.00E−05	0	0	0	0	0	0
BEAG	0	0	0	0	2.00E−05	0	0	0	0	0
BEAC	0	0	0	0	0	0	0	0	0	0
BMD	0	0	0	0	0	0	0	0	0	0
BICH	0	0	0	0	0	0	0	0	0	0
BORZ	0.00012	0	0	0	0	0	0	0	0	0
BOX	0	0	0	0	0	0	0	0	0	0
BULM	0.0001	0	0	0	0	0	0	0	0	0
ACKR	0	0	0	0	0	0	0	0	0	0
DACH	0.99971	4.00E−05	0.99837	0.99993	0.99805	0.99999	0.99689	0.99999	0.99998	0.66498
DALM	0	0	0	0	0	0	0	0	0	0
ESPR	0	0	0	0	0	0	0	0	0	0
FSP	0	0	0	0	0	0	0	0	0	0
FCR	0	0	0	0	2.00E−05	0	0	0	0	0
EFOX	0	0	0	0	0	0	0	0	0	0
FBLD	0	0	0	0	0	0	0	0	0	0
GPIN	0	0	0	0	0	0	0	0	0	0
GSHP	0	0	0	0	0	0	0	0	0	0
GOLD	0	0	0.00162	0	0.00188	0	0.00308	0	1.00E−05	1.00E−05
IBIZ	0	0	0	0	0	0	0	0	0	0
IRSE	1.00E−05	0	0	0	0	0	0	0	0	0
IRWS	0	0	0	0	0	0	0	0	0	0
LAB	2.00E−05	0	0	0	0	0	0	0	0	0
MAST	0	0	0	0	0	0	0	0	0	0
PBGV	0	0	0	0	0	0	0	0	0	0
PAPI	0	0	0	0	0	0	0	0	0	0
PTWD	0	0	0	0	0	0	0	0	0	0
ROTT	0	0.99994	0	0	0	0	1.00E−05	0	0	0.33498
STBD	0	0	0	0	0	0	0	0	0	0
SCDH	0	0	0	0	0	0	0	0	0	0
SPIN	0	0	0	0	0	0	0	0	0	0
SCOL	0	0	0	0	0	0	0	0	0	0
SSCH	0	0	0	0	0	0	0	0	0	0
WSSP	0	0	0	0	0	0	0	0	0	0

TABLE 21F

Canid population*	GOLD Canid Identification Number (missing genotypes) 816 (0)	807 (1)	50 (10)	614 (16)	18477 (26)	591 (7)	592 (14)	593 (22)	603 (27)	604 (4)
AHTR	0	0	0	0	0	0	0	0	0	0
AMWS	0	0	0	0	0	0	0	0	0	0
BASS	0	0	0	0	0	0	0	0	0	0

TABLE 21F-continued

Canid population*	GOLD Canid Identification Number (missing genotypes) 816 (0)	807 (1)	50 (10)	614 (16)	18477 (26)	591 (7)	592 (14)	593 (22)	603 (27)	604 (4)
BEAG	0	0	6.00E−05	0	0	0	0	0	0	0
BEAC	0	0	0	0	0	0	0	0	0	0
BMD	0	0	0	0.19213	0	0	0	0	0	0
BICH	0	0	0	0	0	0	0	0	0	0
BORZ	0	0	0	0	0	0	0	0	0	0
BOX	0	0	0	0	0	0	0	0	0	0
BULM	1.00E−05	0	0	0	0	0	0.00011	0	0	0
ACKR	0	0	0	0	0	0	0	0	0	0
DACH	0	0	0.7605	7.00E−05	0	0	0	0.00999	0.00015	0
DALM	0	0	0	0	0	0	0	0	0	0
ESPR	0	0	0	0	0	0	0	0	0	0
FSP	0	0	0	0	0	0	0	0	0	0
FCR	0	0	0	0	0	0	0	0	0	0
EFOX	0	0	0	0	0	0	0	0	0	0
FBLD	0	0	0	0	0	0	0	0	0	0
GPIN	0	0	0	0	0	0	0	0	0	0
GSHP	0	0	0	0	0	0	0	0	0	0
GOLD	0.99998	0.99999	0.23937	0.80778	0.99999	0.78123	0.99987	0.99	0.99984	0.99979
IBIZ	0	0	3.00E−05	0	0	0	0	0	0	0
IRSE	0	0	0	0	0	0	0	0	0	
IRWS	0	0	0	0	0	0	0	0	0	0
LAB	0	0	0	0	0	0	0	0	0	0
MAST	0	0	0	0	0	0	0	0	0	0
PBGV	0	0	0	0	0	0	0	0	0	0
PAPI	0	0	0	0	0	0	0	0	0	0
PTWD	0	0	0	0	0	0	0	0	0	0
ROTT	0	0	0	0	0	0.21876	0	0	0	0.0002
STBD	0	0	0	0	0	0	0	0	0	0
SCDH	0	0	0	0	0	0	0	0	0	0
SPIN	0	0	0	0	0	0	0	0	0	0
SCOL	0	0	0	0	0	0	0	0	0	0
SSCH	0	0	0	0	0	0	0	0	0	0
WSSP	0	0	0	0	0	0	0	0	0	0

TABLE 21G

Canid population*	ROTT Canid Identification Number (missing genotypes) 817 (2)	818 (2)	886 (2)	896 (0)	22720 (15)	1014 (14)	1028 (0)	1029 (26)	1033 (79)	1034 (0)
AHTR	0	0	0	0	0	0	0	0	0	0
AMWS	0	0	0	0	0	0	0	0	0	0
BASS	0	0	0	0	0	0	0	0	0	0
BEAG	0	0	0	0	0	2.00E−05	0	0	0	0
BEAC	0	0	0	0	0	0	0	0	0	0
BMD	0	0	0	0	0	0	0	0	0	0
BICH	0	0	0	0	0	0	0	0	0	0
BORZ	0	0	0	0	0	0	0	0	0	0
BOX	0	0	0	0	0	0	0	0	0	0
BULM	0	0	0	0	0	0	0	0	0	0
ACKR	0	0	0	0	0	0	0	0	0	0
DACH	0	0	0	0	0	0.0017	0	0	0.00056	0
DALM	0	0	0	0	0	0	0	0	0	0
ESPR	0	0	0	0	0	0	0	0	0	0
FSP	0	0	0	0	0	0	0	0	0	0
FCR	0	0	0	0	0	0	0	0	0	0
EFOX	0	0	0	0	0	0	0	0	0	0
FBLD	0	0	0	0	0	0	0	0	0	0
GPIN	0	0	0	0	0	0	0	0	0	0
GSHP	0	0	0	0	0	0	0	0	0	0
GOLD	0.02636	0	0	0	0	5.00E−05	0	0	0	0
IBIZ	0	0	0	0	0	0	0	0	0	0
IRSE	0	0	0	0	0	0	0	0	0	0
IRWS	0	0	0	0	0	0	0	0	0	0
LAB	0	0	0	0	0	0	0	0	0	0
MAST	3.00E−05	0	0	0	0	0	0	0	0	0
PBGV	0	0	0	0	0	0	0	0	0	0
PAPI	0	0	0	0	0	0	0	0	0	0

TABLE 21G-continued

	ROTT Canid Identification Number (missing genotypes)									
Canid population*	817 (2)	818 (2)	886 (2)	896 (0)	22720 (15)	1014 (14)	1028 (0)	1029 (26)	1033 (79)	1034 (0)
PTWD	0	0	0	0	0	0	0	0	0	0
ROTT	0.97359	0.99999	0.99999	0.99999	0.99999	0.9982	0.99999	0.99998	0.99943	0.99999
STBD	0	0	0	0	0	0	0	0	0	0
SCDH	0	0	0	0	0	0	0	0	0	0
SPIN	0	0	0	0	0	0	0	0	0	0
SCOL	0	0	0	0	0	0	0	0	0	0
SSCH	0	0	0	0	0	0	0	0	0	0
WSSP	0	0	0	0	0	0	0	0	0	0

TABLE 21H

	MAST Canid ID NO (missing genotypes)						SCOL Canid ID NO (missing genotypes)		
Canid population[a]	23967 (14)	991 (6)	1015 (9)	1016 (11)	992 (1)	1013 (80)	15628 (24)	375 (12)	363 (12)
AHTR	0	0	0	0	0	0	0	0	0
AMWS	0	0	0	0	0	0	0	0	0
BASS	0	0	0	0	0	0	0	0	0
BEAG	0	0	0	0	0	0	0	0	0
BEAC	0	0	0	0	0	0	0	0	0
BMD	0	0	0	0	0	0	0	0	0
BICH	0	0	0	0	0	0	0	0	0
BORZ	0	0	0	0	0	0	0	0	0
BOX	0	0	0	0	0	0	0	0	0
BULM	0	0	0	0	0	3.00E−05	0	4.00E−05	0
ACKR	0	0	0	0	0	0	0	0	0
DACH	0	0	0	0	0	0	0.00413	0	0.00057
DALM	0	0	0	0	0	0	0	0	0
ESPR	0	0	0	0	0	0	0	0	0
FSP	0	0	0	0	0	0	0	0.00503	0
FCR	0	0	0	0	0	0	0	0	0
EFOX	0	0	0	0	0	0	0	0	0
FBLD	0	0	0	0	0	0	9.00E−05	1.00E−05	0
GPIN	0	0	0	0	0	0	0	0	0
GSHP	0	0	0	0	0	0	0	0	0
GOLD	0.00012	0	0	0	0.00146	0	4.00E−05	0.00043	0.00105
IBIZ	0	0	0	0	0	0	0	0	0
IRSE	0	0	0	0	0	0	0	0	0
IRWS	0	0	0	0	0	0	0	0	0
LAB	0	0	0	0	0	0	0	0	0
MAST	0.99987	0.99999	0.99999	0.99999	0.99852	0.99995	0	0	0
PBGV	0	0	0	0	0	0	0	0	0
PAPI	0	0	0	0	0	0	0	0	0
PTWD	0	0	0	0	0	0	0	0	0
ROTT	0	0	0	0	0	0	0	0	0
STBD	0	0	0	0	0	0	0	0	0
SCDH	0	0	0	0	0	0	0	0	0
SPIN	0	0	0	0	0	0	0	0	0
SCOL	0	0	0	0	0	0	0.99572	0.99445	0.99837
SSCH	0	0	0	0	0	0	0	0	0
WSSP	0	0	0	0	0	0	0	0	0

[a] See Table 5 for abbreviations of canid populations.
KBB: pbe

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<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 16

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<210> SEQ ID NO 17
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<223> OTHER INFORMATION: Oligonucleotide Primer

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<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 24

tgaggctccg tgggtatgtg 20

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<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 25

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<210> SEQ ID NO 26
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<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 26

tgccctcaaa caatttgc 18

<210> SEQ ID NO 27
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<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 27

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tcgggatgtt tctcttccac 20

<210> SEQ ID NO 28
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<400> SEQUENCE: 28

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caacccaggg tggaagc 17

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<400> SEQUENCE: 30

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<220> FEATURE:
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<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 36

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<210> SEQ ID NO 37
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<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 37

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<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 38

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<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 39

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<210> SEQ ID NO 40
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<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

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<400> SEQUENCE: 41

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<400> SEQUENCE: 42

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<400> SEQUENCE: 43

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<400> SEQUENCE: 44

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<223> OTHER INFORMATION: Oligonucleotide Primer

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<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 48

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<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 49

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<210> SEQ ID NO 50
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 50

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 51

aaggcaggag gaggagcac                                                   19


<210> SEQ ID NO 52
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 52

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<210> SEQ ID NO 53
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 53

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<210> SEQ ID NO 54
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<211> LENGTH: 19
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 54

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<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 55

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<210> SEQ ID NO 56
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 56

aggctctccg agggtaagac 20

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<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

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ggctggactt ttgtcatttg 20

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<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 58

cttcccatta tagccctgtc c 21

<210> SEQ ID NO 59
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 59

tccctcctga cactgcttta 20

<210> SEQ ID NO 60
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 60

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ccccttttgca ctactgttga g                                              21


<210> SEQ ID NO 61
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 61

ttctcgtgac ccctaaagga                                                 20


<210> SEQ ID NO 62
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 62

aaacaagaca gtaggaagag agg                                             23


<210> SEQ ID NO 63
<211> LENGTH: 20
<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 63

tgggagcttc atacaaatgc                                                 20


<210> SEQ ID NO 64
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 64

aattactcgg cctctctggg                                                 20


<210> SEQ ID NO 65
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 65

gtgatccact tgcttgtatc c                                               21


<210> SEQ ID NO 66
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<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 66

catgcctgac tcaactgatg                                                 20


<210> SEQ ID NO 67
<211> LENGTH: 19
<212> TYPE: DNA
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 67

ggggctctgt tattaggtg                                                   19


<210> SEQ ID NO 68
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<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 68

tgacttactc tagccacttt t                                                21


<210> SEQ ID NO 69
<211> LENGTH: 20
<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 69

ttacatttag gggctccagt                                                  20


<210> SEQ ID NO 70
<211> LENGTH: 20
<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 70

gccttctttg gaaaaacacc                                                  20


<210> SEQ ID NO 71
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<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 71

acacatttgt gtgcttgtct tg                                               22


<210> SEQ ID NO 72
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<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 72

acaagccgac tctagcgaaa                                                  20


<210> SEQ ID NO 73
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 73

ggtcccatcc tcaaaatcct c                                                21
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<211> LENGTH: 19
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 74

atttgccagg taccattcc                                                    19


<210> SEQ ID NO 75
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 75

gcagacgagc acaccgaa                                                     18


<210> SEQ ID NO 76
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<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 76

aatatgggag aggagaagag gg                                                22


<210> SEQ ID NO 77
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 77

tggctgtggc taaggctttg t                                                 21


<210> SEQ ID NO 78
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<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 78

ccctctactt atgtctcggc c                                                 21


<210> SEQ ID NO 79
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 79

ccaagaacag cctaagctgg                                                   20


<210> SEQ ID NO 80
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<212> TYPE: DNA
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<220> FEATURE:
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<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 80

cagctggatt ggggactc                                                   18


<210> SEQ ID NO 81
<211> LENGTH: 18
<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 81

ccgatgcctg tcctttga                                                   18


<210> SEQ ID NO 82
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 82

agtacttgag gcttggagtc ag                                              22


<210> SEQ ID NO 83
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 83

atggcaggtc aagagtatgg                                                 20


<210> SEQ ID NO 84
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 84

ttcattggct ggtgactttg                                                 20


<210> SEQ ID NO 85
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 85

agtaaagggt tctcaagtgt gc                                              22


<210> SEQ ID NO 86
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 86

cagttcatcc ttcccctct c                                                21
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<210> SEQ ID NO 87
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 87

gattaaaagg gcaagcaacc                                                20


<210> SEQ ID NO 88
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 88

cagtgagcaa agcaaatgaa                                                20


<210> SEQ ID NO 89
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 89

aaggtagtcc cacgatcctc                                                20


<210> SEQ ID NO 90
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 90

tgatacccat taagtccatc c                                              21


<210> SEQ ID NO 91
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 91

ccaatattgt taagaagttc aagc                                           24


<210> SEQ ID NO 92
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 92

cctctagatc catccatatt gtca                                           24


<210> SEQ ID NO 93
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer
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<400> SEQUENCE: 93

aatggtggtg atattcacag aga                                              23


<210> SEQ ID NO 94
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 94

aggcagagct aaacctgagc                                                  20


<210> SEQ ID NO 95
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 95

gaaattgttc catttctgtg acat                                             24


<210> SEQ ID NO 96
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 96

tacatctcca catctactga                                                  20


<210> SEQ ID NO 97
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 97

atggcccacc gatacaca                                                    18


<210> SEQ ID NO 98
<211> LENGTH: 16
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 98

ttccccaagc cacacc                                                      16


<210> SEQ ID NO 99
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 99

cagcaattgg acaagaaaaa g                                                21


<210> SEQ ID NO 100
<211> LENGTH: 19
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 100

cagcgaattt gggcactaa                                                    19


<210> SEQ ID NO 101
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 101

ccattcgcca caagtaggtt                                                   20


<210> SEQ ID NO 102
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 102

ttccagactg ctgcctcc                                                     18


<210> SEQ ID NO 103
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 103

ccccaaatac atccctacat                                                   20


<210> SEQ ID NO 104
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 104

cgtgctttgt tatggcttga                                                   20


<210> SEQ ID NO 105
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 105

tacccataaa gttgggcttg                                                   20


<210> SEQ ID NO 106
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 106
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ctttcttccg ccactacctg                                                   20


<210> SEQ ID NO 107
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 107

aatggcaagg atgctactcc                                                   20


<210> SEQ ID NO 108
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 108

actggacact tcttttcaga cg                                                22


<210> SEQ ID NO 109
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 109

actcattttc tcttattctg cag                                               23


<210> SEQ ID NO 110
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 110

gctctcatcc ctgtgaaagc                                                   20


<210> SEQ ID NO 111
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 111

aaaaacccac aacaaagtgc                                                   20


<210> SEQ ID NO 112
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 112

caagggttag cacctgggta                                                   20


<210> SEQ ID NO 113
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 113

gggtgtgaaa acagccaact                                                 20


<210> SEQ ID NO 114
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 114

tggcatattc aacaaattgc                                                 20


<210> SEQ ID NO 115
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 115

ctgggtggtt cagtagttgg                                                 20


<210> SEQ ID NO 116
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 116

aagctgagcc attcttttcc                                                 20


<210> SEQ ID NO 117
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 117

ttgcagccta ttgtggactt t                                               21


<210> SEQ ID NO 118
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 118

cacaccagct cgtcctcata a                                               21


<210> SEQ ID NO 119
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 119

ggctgtggtt tgtccttgtt                                                 20
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<210> SEQ ID NO 120
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 120

ttgggtttca cactcagcag                                                  20


<210> SEQ ID NO 121
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 121

ggcacagaat ccaacttgag                                                  20


<210> SEQ ID NO 122
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 122

cagggccatt ggtctagaaa                                                  20


<210> SEQ ID NO 123
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 123

ccccaaaaaa tccaacca                                                    18


<210> SEQ ID NO 124
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 124

aggccaaggg aatgatgctc                                                  20


<210> SEQ ID NO 125
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 125

gggagtgggg gaaataaatg                                                  20


<210> SEQ ID NO 126
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer
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<400> SEQUENCE: 126

atcatcctag cactcagaag g                                               21


<210> SEQ ID NO 127
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 127

ctgcttaaat tctcccagcg                                                 20


<210> SEQ ID NO 128
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 128

agcatcaatt agatgtcagc g                                               21


<210> SEQ ID NO 129
<211> LENGTH: 19
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 129

tagcaagaaa atgtgccca                                                  19


<210> SEQ ID NO 130
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 130

tcctttgaat tagcacttgg c                                               21


<210> SEQ ID NO 131
<211> LENGTH: 19
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 131

tccaggaagt gtctgcagg                                                  19


<210> SEQ ID NO 132
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 132

tggattatta aggggaattt agc                                             23


<210> SEQ ID NO 133
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<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 133

acgtcgagct cctggcat                                                  18


<210> SEQ ID NO 134
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 134

aacagcattt cagacagagg                                                20


<210> SEQ ID NO 135
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 135

aaacggagtt ccatctctgg                                                20


<210> SEQ ID NO 136
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 136

cctatgcagg gtaggcacat                                                20


<210> SEQ ID NO 137
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 137

tcttcaaaga aaaccaacag g                                              21


<210> SEQ ID NO 138
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 138

gttctccaaa gcactcat                                                  18


<210> SEQ ID NO 139
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 139
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acaccaaatg tgtgaaggca                                                  20


<210> SEQ ID NO 140
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 140

ggggacaaat ttccactcct                                                  20


<210> SEQ ID NO 141
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 141

atggagcatg ggtgagaaat                                                  20


<210> SEQ ID NO 142
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 142

atcctggtat caaatctatc a                                                21


<210> SEQ ID NO 143
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 143

aatagactat gtaactgtct ctggc                                            25


<210> SEQ ID NO 144
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 144

gcaatggaaa gaggatggaa                                                  20


<210> SEQ ID NO 145
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 145

gttgattggg agataatcca ca                                               22


<210> SEQ ID NO 146
<211> LENGTH: 23
<212> TYPE: DNA
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 146

ttagagctta ctcatgatat ctg                                             23


<210> SEQ ID NO 147
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 147

cctggattat aagcatgaga gc                                              22


<210> SEQ ID NO 148
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 148

tttctgagcc acttttccat ag                                              22


<210> SEQ ID NO 149
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 149

gggggtgtcg gtggagttct                                                 20


<210> SEQ ID NO 150
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 150

gccacctcat tccaaaaaga                                                 20


<210> SEQ ID NO 151
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 151

tatggagatg gagggcacac                                                 20


<210> SEQ ID NO 152
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 152

atgaggaggt gcaactatcc                                                 20
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<210> SEQ ID NO 153
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 153

caggctttgt tgaggtgtca                                                20


<210> SEQ ID NO 154
<211> LENGTH: 19
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 154

aacactgaca tgcatccac                                                 19


<210> SEQ ID NO 155
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 155

tggtggataa atagataagg a                                              21


<210> SEQ ID NO 156
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 156

attgcttgga taagaggggg                                                20


<210> SEQ ID NO 157
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 157

tgtgagtagg gtagggcaag                                                20


<210> SEQ ID NO 158
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 158

ggtgtcagga aaatgagacc a                                              21


<210> SEQ ID NO 159
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 159

aggcctgctg tttctcttct                                         20


<210> SEQ ID NO 160
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 160

tcccttttg tggctgaa                                            18


<210> SEQ ID NO 161
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 161

ggcataaatt gtctttgccc                                         20


<210> SEQ ID NO 162
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 162

caagattcaa aacaagcaac c                                       21


<210> SEQ ID NO 163
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 163

ccatggagag tggttattgc                                         20


<210> SEQ ID NO 164
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 164

aatgacattg agcctgggaa                                         20


<210> SEQ ID NO 165
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 165

atagccttgg gaatttttgc                                         20
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<210> SEQ ID NO 166
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 166

tatggacctt cgttcagagg                                                   20


<210> SEQ ID NO 167
<211> LENGTH: 19
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 167

tcataaggca aagaaaacc                                                    19


<210> SEQ ID NO 168
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 168

ttgtcccttg tataactgat g                                                 21


<210> SEQ ID NO 169
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 169

ttagacaaaa taggcttcaa                                                   20


<210> SEQ ID NO 170
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 170

ttcagggaat tctttcttgg                                                   20


<210> SEQ ID NO 171
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 171

ttgtatggag gtggggagag                                                   20


<210> SEQ ID NO 172
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer
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<400> SEQUENCE: 172

agatggggcc taaccaaagt                                                  20


<210> SEQ ID NO 173
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 173

cccttctggc ctcctacaca                                                  20


<210> SEQ ID NO 174
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 174

caggttattc tgggctatgg                                                  20


<210> SEQ ID NO 175
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 175

tattccacat cattcacc                                                    18


<210> SEQ ID NO 176
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 176

atgcttcctg gtaagcaatc a                                                21


<210> SEQ ID NO 177
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 177

ccccttccag cttcggtgta g                                                21


<210> SEQ ID NO 178
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 178

gagaggagaa acaaccaaca cc                                               22


<210> SEQ ID NO 179
<211> LENGTH: 20
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 179

acacatacac gcccaattca                                                  20


<210> SEQ ID NO 180
<211> LENGTH: 17
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 180

catcttgctc tctcaac                                                     17


<210> SEQ ID NO 181
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 181

acctggcctc ttctgttgtc t                                                21


<210> SEQ ID NO 182
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 182

caagctgaga gccatgtagg                                                  20


<210> SEQ ID NO 183
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 183

gatagatcca agccaacacc                                                  20


<210> SEQ ID NO 184
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 184

ccccaggacc atttgttaga                                                  20


<210> SEQ ID NO 185
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 185
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catttgtcat tgtggaaaac c                                                    21


<210> SEQ ID NO 186
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 186

gtgctagtct ggctgtgctc a                                                    21


<210> SEQ ID NO 187
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 187

tcatctccag cttttcatgg                                                      20


<210> SEQ ID NO 188
<211> LENGTH: 19
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 188

atgtgaaccc cgcccaata                                                       19


<210> SEQ ID NO 189
<211> LENGTH: 19
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 189

gagccctgtt ctcaggttg                                                       19


<210> SEQ ID NO 190
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 190

caataccctg ataccaaaac c                                                    21


<210> SEQ ID NO 191
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 191

aggccttctc tgtcctcttg                                                      20


<210> SEQ ID NO 192
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 192

tgtccaccca cagatgaatg                                                20


<210> SEQ ID NO 193
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 193

ggatgcttgg gaatcttgaa                                                20


<210> SEQ ID NO 194
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 194

tacaggcact ccttcctacg                                                20


<210> SEQ ID NO 195
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 195

aggtttgggc tcctcattct                                                20


<210> SEQ ID NO 196
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 196

gagacttaac acagtatttg                                                20


<210> SEQ ID NO 197
<211> LENGTH: 19
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 197

tcggggacat acttgaacc                                                 19


<210> SEQ ID NO 198
<211> LENGTH: 19
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 198

aaccactatc caactttat                                                 19
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<210> SEQ ID NO 199
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 199

gaaagaggat gaagggtgtg 20

<210> SEQ ID NO 200
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 200

caactaaggc agagaatacc a 21

<210> SEQ ID NO 201
<211> LENGTH: 19
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 201

cacgacgttg taaaacgac 19

<210> SEQ ID NO 202
<211> LENGTH: 337
<212> TYPE: DNA
<213> ORGANISM: canine genomic DNA
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(337)
<223> OTHER INFORMATION: Wherein N = A or C or G or T
<220> FEATURE:
<221> NAME/KEY: allele
<222> LOCATION: (82)..(82)
<223> OTHER INFORMATION: C to T
<220> FEATURE:
<221> NAME/KEY: allele
<222> LOCATION: (133)..(133)
<223> OTHER INFORMATION: T to C

<400> SEQUENCE: 202

gcttttggac aactttggat agactccttt ctctggaatg acttccagca tatggtgcag 60

cttcaaggcc agagaagaga ccagatgacc tttcaagtgt ccttccagtc caaagnnnnn 120

nnnttccaat actgagggtt ttcaaactgg tgttggtatt tgcttttcaa agagagacag 180

actgagtttc tcatatcaaa tccctatagc ctcataaaag cacttttcag ttttattttc 240

catcagaaat tcctatgaaa agcatttgaa gtttcaaaag ctccctacac ccaagnngct 300

gattgagatt ttagcccaga gagtgacgta gatcaca 337

<210> SEQ ID NO 203
<211> LENGTH: 341
<212> TYPE: DNA
<213> ORGANISM: canine genomic DNA
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(341)
<223> OTHER INFORMATION: Wherein N = A or C or G or T
<220> FEATURE:
<221> NAME/KEY: allele

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<222> LOCATION: (285)..(285)
<223> OTHER INFORMATION: G to A

<400> SEQUENCE: 203

gaattccaaa tgtcctgctt agggtccagc aggatagagg gatagnnnnn nnnnnnntga     60

ggtaggagga aacagtgact tttccagaaa cagtgcaaca tttctcctgc atttttaacc    120

tctatagatg atactcattt ctcattagcc agagttcctg cattccattg gcagtaagtt    180

gtccatcaga atccctgaaa nnacaacttt gggtgaactg gaagccattc acactttgcc    240

agttgggtaa tgccagttag tacatacctt tctcataagg ttttgaatac ctgnnnnnnn    300

nnnnnnncca atgaataccc acacccttgg tagatgaaag a                        341


<210> SEQ ID NO 204
<211> LENGTH: 302
<212> TYPE: DNA
<213> ORGANISM: canine genomic DNA
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(302)
<223> OTHER INFORMATION: Wherein N = A or C or G or T
<220> FEATURE:
<221> NAME/KEY: allele
<222> LOCATION: (50)..(50)
<223> OTHER INFORMATION: Deletion A
<220> FEATURE:
<221> NAME/KEY: allele
<222> LOCATION: (93)..(93)
<223> OTHER INFORMATION: C to G
<220> FEATURE:
<221> NAME/KEY: allele
<222> LOCATION: (128)..(128)
<223> OTHER INFORMATION: C to G
<220> FEATURE:
<221> NAME/KEY: allele
<222> LOCATION: (257)..(257)
<223> OTHER INFORMATION: C to T
<220> FEATURE:
<221> NAME/KEY: allele
<222> LOCATION: (271)..(271)
<223> OTHER INFORMATION: G to T

<400> SEQUENCE: 204

aagcatactt ccctgaaatg aggcttcact atctgatttg ctttggctaa taaatataaa     60

tagaagtgag atgggtcact tctaggctgt agctttaagg gcaggatgtg tgtcgctaaa    120

ttctcctctt ctcctgccat aatgactgac atcagnnntt ctccatcagc ttggggcctg    180

aagtgtaatg atgtagagaa gaaccaggct tatgtaagtg aggaataaac aaccttgtta    240

gaaactacag atatggcggt gtttattact gcagcataat ccaacacttt atggctgata    300

ca                                                                   302


<210> SEQ ID NO 205
<211> LENGTH: 408
<212> TYPE: DNA
<213> ORGANISM: canine genomic DNA
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(408)
<223> OTHER INFORMATION: Wherein N = A or C or G or T
<220> FEATURE:
<221> NAME/KEY: allele
<222> LOCATION: (5)..(57)
<223> OTHER INFORMATION: T to C

<400> SEQUENCE: 205

agtcaaatcg ttcattggat tcccttgcac tcagagctta tgagaagagc tgacaatgta     60
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ctcagcagcc gtgtccttct tcctaaatta ttggctttta tttcatcaga gtgaaagccc 120

ttnnnnnnnc agggtttgaa attgccatca cttcaaattt cctataagca cttcttgcat 180

gtgaatgttt actgaatgca gttaactgtt ttctaaattt aactagcttt aacgaatttg 240

attttcaaac tgaaaaagaa ataattgatg tcaatttcat ttcaattcca caaagagaat 300

ggggggtggg caatgcagaa atcatgtcct gaagcattta cttttatttt ttaatttttt 360

aaagatttgt ttatttgaga gacagagaga gggagtacat tcaagcag 408

<210> SEQ ID NO 206
<211> LENGTH: 381
<212> TYPE: DNA
<213> ORGANISM: canine genomic DNA
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(381)
<223> OTHER INFORMATION: Wherein N = A or C or G or T
<220> FEATURE:
<221> NAME/KEY: allele
<222> LOCATION: (156)..(156)
<223> OTHER INFORMATION: Insert T
<220> FEATURE:
<221> NAME/KEY: allele
<222> LOCATION: (258)..(258)
<223> OTHER INFORMATION: C to T
<220> FEATURE:
<221> NAME/KEY: allele
<222> LOCATION: (303)..(303)
<223> OTHER INFORMATION: C to T
<220> FEATURE:
<221> NAME/KEY: allele
<222> LOCATION: (312)..(312)
<223> OTHER INFORMATION: Insert A

<400> SEQUENCE: 206

aaaaggtggc acatatgaaa agttgttgtt tttttttttc ctaatgtcat ggcctgtcac 60

ttagacaaaa agcataatga gggaagtttc taagaattat annnnnnnnn nngctaatca 120

aattttaagg aatgtatatg gtggtgaggt gaaggatcaa gatggcagtt gtttgcaaag 180

gaaaggaagg tggaaataaa ggagtatcca agagggataa tataacaaaa aattattgag 240

tttcagagaa atcaggtgaa tggaagatgt aacagggctc taacatgaan ntggtccaag 300

nngattcaac ataaaaatta ccagtcatgg gtgcctgagt tgttcaaagt cagttaagcc 360

tcccttaagc ctctgactct t 381

<210> SEQ ID NO 207
<211> LENGTH: 344
<212> TYPE: DNA
<213> ORGANISM: canine genomic DNA
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(344)
<223> OTHER INFORMATION: Wherein N = A or C or G or T
<220> FEATURE:
<221> NAME/KEY: allele
<222> LOCATION: (254)..(254)
<223> OTHER INFORMATION: G to A

<400> SEQUENCE: 207

ggggtttcta ttccattttc accacgtttg aaggacaaat tgaggctgcc ctcatacaaa 60

tgcccctggg cnnnnnnatt agggttgggg ttgggggnnn nnnnnnnngg ccagaattcc 120

tctctcaccc aacaggggag gcagtaatgc cttattttgc cgtcttgggt ggtgacagta 180

gtgagagctt ggttctgggg ctaaacagag acagccttgc caacagatgt cagctcacca 240

gaagtggtca agcgtttctc aaagtagcca cagtgctggg agcagccaag gctttcnnnn 300

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nnnnannatn gaaactcaaa ctgtgtcaac agtatgcatt ccaa 344

<210> SEQ ID NO 208
<211> LENGTH: 370
<212> TYPE: DNA
<213> ORGANISM: canine genomic DNA
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(370)
<223> OTHER INFORMATION: Wherein N = A or C or G or T
<220> FEATURE:
<221> NAME/KEY: allele
<222> LOCATION: (165)..(165)
<223> OTHER INFORMATION: G to C

<400> SEQUENCE: 208

acctcatgta tgtcttgttc cccaagaacc cttcgtccag ggattttttt tttaaatgta 60

tttattcatg agagacagag agagagagag agaatggggc agagacacag gcagagggag 120

aagcaggctc cacacnnnnn nnnnnnngtg gggactcgat cccgggtctc caggatcagg 180

ccctggactg aaggtagtgc taaaccgctg agccacctgg gctgcccagc ctaatctttt 240

ttgttgttgt tgttttgttt tgttttttta agattctatt tattttagag agagagggtt 300

aaaaaaactt tagcagactc catgctcagc acnngcccca tgagggctcg atctcaggac 360

cccaagatca 370

<210> SEQ ID NO 209
<211> LENGTH: 337
<212> TYPE: DNA
<213> ORGANISM: canine genomic DNA
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(337)
<223> OTHER INFORMATION: Wherein N = A or C or G or T
<220> FEATURE:
<221> NAME/KEY: allele
<222> LOCATION: (66)..(66)
<223> OTHER INFORMATION: T to A

<400> SEQUENCE: 209

ctctgctagg agaaaaggag agaaactact gcttttccta tggattttaa cctccacctt 60

tcaatttttt cccctgggta agggacaggg taggattgga acagngggca ggcagattgt 120

nnnnnnnnnn tatctgggat tgaatatggg ttgtaatagc tttagaaatt gtcatttctc 180

ttgccttgac cagccagttt tctgggaagt agaggatatg aaagcatttg tgctcttcca 240

gaataagatg tgtattcatg aaattagttg ttgctcttaa ataaaatgct tccttatgta 300

caaaattctc nagcaggctg aatggactga attgtgt 337

<210> SEQ ID NO 210
<211> LENGTH: 480
<212> TYPE: DNA
<213> ORGANISM: canine genomic DNA
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(480)
<223> OTHER INFORMATION: Wherein N = A or C or G or T
<220> FEATURE:
<221> NAME/KEY: allele
<222> LOCATION: (384)..(384)
<223> OTHER INFORMATION: A to G

<400> SEQUENCE: 210

caaatggttc aagaggagat tcttgtaata gttctgctat tggcaaggtg gtaggaggag 60

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gctttcagga cacagcagca aggtgtttta nnnnnnnnnn nctcactgtg ttatggctct 120

cctgaggttc cagtccattg ggagtatatg ggtgaaacct taaatctcaa agggatcttc 180

cttaagactg acatgtacta tagtcagtca cttgatacat gaggcagatg acccagacaa 240

aagtggctac tactagggtg tccacatatg gctacacagt agaatcacct ggagagcttt 300

tacgatccca gtgcccaagt cataacctat tcaaattaaa ttacagtgtt ggggcnnnga 360

gtcagatagc aatatttttt aaagacccca gctgattcca gtgcattgca ccttttgcaa 420

ctaatgggct tatgatttat ctaacatcac acaagtgggg acaggaacct acaatggtta 480

<210> SEQ ID NO 211
<211> LENGTH: 313
<212> TYPE: DNA
<213> ORGANISM: canine genomic DNA
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(313)
<223> OTHER INFORMATION: Wherein N = A or C or G or T
<220> FEATURE:
<221> NAME/KEY: allele
<222> LOCATION: (88)..(88)
<223> OTHER INFORMATION: T to C
<220> FEATURE:
<221> NAME/KEY: allele
<222> LOCATION: (138)..(138)
<223> OTHER INFORMATION: C to A
<220> FEATURE:
<221> NAME/KEY: allele
<222> LOCATION: (266)..(266)
<223> OTHER INFORMATION: T to G

<400> SEQUENCE: 211

aaagtaaaat caggtattct cctcctaact atgaaganan nntaattttt agagtgaaat 60

ctgagttaac aactcctaca atcacaatct tgtttgccaa tccagcgtta tgagctgccc 120

atcccagaag aaaaaaactn nnnnnnnttg tggtgttatg aaatgagcct gcctatggac 180

tccaaaaaaa gctagatcca gggtgcaatg tccatctttg gtcatgccta tcccctcatt 240

ccagtaattg accaacattt aggagttagt gtttttcccc tatgcttact acttcagata 300

gatatgcatg cca 313

<210> SEQ ID NO 212
<211> LENGTH: 353
<212> TYPE: DNA
<213> ORGANISM: canine genomic DNA
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(353)
<223> OTHER INFORMATION: Wherein N = A or C or G or T
<220> FEATURE:
<221> NAME/KEY: allele
<222> LOCATION: (317)..(317)
<223> OTHER INFORMATION: T to A

<400> SEQUENCE: 212

caccctcaag aagttaaagc acaactcttc accccttaag tatgggctac acagtgactt 60

ccttcgaaag aggacagttt gggaaggggg aaaaacagga nnnnnnnnnn ngagaagcct 120

aataaatact atcttagcca ggtgactaag gctggcaaca tcaagagcta tgtcaaataa 180

catatgccct tgatataata tgataagaat ggcactgtag acttcctccc tcaaatcctt 240

aaccactatc taatcatgag aaaaatatta gacaaccaaa attgaaggac atactacaaa 300

atatctaact actacttctc aaaaccgtca annccagtct tctcaaaacc agg 353

<210> SEQ ID NO 213
<211> LENGTH: 336
<212> TYPE: DNA
<213> ORGANISM: canine genomic DNA
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(336)
<223> OTHER INFORMATION: Wherein N = A or C or G or T
<220> FEATURE:
<221> NAME/KEY: allele
<222> LOCATION: (58)..(58)
<223> OTHER INFORMATION: G to C
<220> FEATURE:
<221> NAME/KEY: allele
<222> LOCATION: (108)..(108)
<223> OTHER INFORMATION: A to T

<400> SEQUENCE: 213

taggggacac agtttctaaa ggctgttcac agtttctaga ggcctcccac agtttctgaa 60

ggacttttgc agctccctga tacatgaggt cctccaatgt ggccaataat ttaatccagn 120

nnnnnnnnnn ngcctctaga gttagtgtgc tagcaagatg gagtcttctg taacataacc 180

taagcacgag aatgacatcc tgtcaccttt tccgtatttt attgctttgc aacaaatcac 240

tggtcctgct caccctcaga gggaggcaga agatacaggg agataactcc taaacactaa 300

gagacaaaga aaatgagggc ttcttacatg tctgtc 336

<210> SEQ ID NO 214
<211> LENGTH: 377
<212> TYPE: DNA
<213> ORGANISM: canine genomic DNA
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(377)
<223> OTHER INFORMATION: Wherein N = A or C or G or T
<220> FEATURE:
<221> NAME/KEY: allele
<222> LOCATION: (129)..(129)
<223> OTHER INFORMATION: G to A
<220> FEATURE:
<221> NAME/KEY: allele
<222> LOCATION: (170)..(170)
<223> OTHER INFORMATION: Insert T

<400> SEQUENCE: 214

tctcaaactg ttgaagacca acagaatgat aaaatcttga aagcaacann nnnnnaaaac 60

attcatcata tacaaaggaa caatgagatt aacaattaac ttctcaaaag agataataga 120

ggccagaagt cagtggatga catattcaaa gtnnnnnnnn nnnnnnnnnn nnctcaacca 180

actgaacaaa acaaaaaatg aagatgaaan ngacacttag gtgactctgt cagnnnaaca 240

tgcttctctt gatcttgggg tcatgagttt gagtgcagag attatttaag gaaataaata 300

aaacctgtat atctttttaa atgaaaatga acatattccc agaaaaagat tgaaagaatt 360

tgttcctagc agagacc 377

<210> SEQ ID NO 215
<211> LENGTH: 312
<212> TYPE: DNA
<213> ORGANISM: canine genomic DNA
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(312)
<223> OTHER INFORMATION: Wherein N = A or C or G or T
<220> FEATURE:
<221> NAME/KEY: allele
<222> LOCATION: (76)..(76)
<223> OTHER INFORMATION: C to T
<220> FEATURE:

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<221> NAME/KEY: allele
<222> LOCATION: (108)..(108)
<223> OTHER INFORMATION: G to A
<220> FEATURE:
<221> NAME/KEY: allele
<222> LOCATION: (229)..(229)
<223> OTHER INFORMATION: G to A
<220> FEATURE:
<221> NAME/KEY: allele
<222> LOCATION: (238)..(238)
<223> OTHER INFORMATION: T to C
<220> FEATURE:
<221> NAME/KEY: allele
<222> LOCATION: (263)..(263)
<223> OTHER INFORMATION: A to G

<400> SEQUENCE: 215

catgtgaccc ttcctatgag actgtcacag aaccagccca cactcgggtt ggccggacct     60

gggtcaatcc tcagccgcca nnnnnnnnnn naggtgcagt gtgcccggag ggagcgatgg    120

cgtgagctaa gcctggggca ctggtatcct ccagcagtga ggagggaggc accccaaaan    180

ntgctttaaa tgatcctaac agaaccccac agcgacagac attagccagg agggaagtga    240

ccaagtaaac ctgaaccgag acaggaggct ttattcaaga tcattctcat caaccaaatt    300

gcctctactt tc                                                        312


<210> SEQ ID NO 216
<211> LENGTH: 316
<212> TYPE: DNA
<213> ORGANISM: canine genomic DNA
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(316)
<223> OTHER INFORMATION: Wherein N = A or C or G or T
<220> FEATURE:
<221> NAME/KEY: allele
<222> LOCATION: (212)..(212)
<223> OTHER INFORMATION: T to C

<400> SEQUENCE: 216

ggaagacccc aactctatta ttgcaggcat gccagtcctc gaggtctgga aatcaaagca     60

ggtaaagttt cagacttgtg tttcattcta acaatcaagt atctcttaaa acatgnnnnn    120

nnnattgtcc tggttcactt ggtgagaaat gctgatgcct cttaggagta ctaggagcta    180

gagcaggggt agtgctctcg ctatccagct tttgtctatt tggtgatcat cagagaaccc    240

aagagaatgc cctgctcacc attagaacta gatgatatta tctgggtgga ttaacaaaat    300

ctgtaaccac agctga                                                    316


<210> SEQ ID NO 217
<211> LENGTH: 423
<212> TYPE: DNA
<213> ORGANISM: canine genomic DNA
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(423)
<223> OTHER INFORMATION: Wherein N = A or C or G or T
<220> FEATURE:
<221> NAME/KEY: allele
<222> LOCATION: (274)..(274)
<223> OTHER INFORMATION: T to C

<400> SEQUENCE: 217

agtcttttgg tcctaaacat ggtagaaaac atctttgttg catttttag aattaatcta     60

ttttaaattg acatattttg catgtaatat atttttcagg tatataaann nnnnnnnnna    120

tatttttata cactgcaaaa gatccccata tctggttaac atttgtcacc ttatatggta    180
```

```
aaaaaaattt tacaaaattt attcttgtga tgaaaactta agatttactc ttagcaactt    240

gcacatatac aatacagtag tagccaactt gctatctgtt atatcttcac tttgttgctg    300

tgtctaagaa gtgacagatg ccagtagagg tgtgggatcc tatatganna aatcccagta    360

tctgacattg cagagccttc tacctgccac ctctgagnca ccagtcagtg aggagtcaca    420

gtg                                                                  423
```

<210> SEQ ID NO 218
<211> LENGTH: 304
<212> TYPE: DNA
<213> ORGANISM: canine genomic DNA
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(304)
<223> OTHER INFORMATION: Wherein N = A or C or G or T
<220> FEATURE:
<221> NAME/KEY: allele
<222> LOCATION: (112)..(112)
<223> OTHER INFORMATION: G to A

<400> SEQUENCE: 218

```
agacacatgc attttcccag ctgacttttt gcacccagtg gctcataatc acaatcacat     60

gttatcaact tgcctcatag acccattttt tcagccnnnn nnnnnnngnc agtgtcacat    120

ctcaatacag tggccagaaa agtggttctt gcccctggtt tgcttaacct gagtatcatg    180

gggaacactg tcttctgaat tctagctgtg tgatctgtgt tcctatttat aaccatgttt    240

tatctttcag acctgacaca actagtctga tttggacatt ttgctcctgt tcacaatgaa    300

gatt                                                                 304
```

<210> SEQ ID NO 219
<211> LENGTH: 316
<212> TYPE: DNA
<213> ORGANISM: canine genomic DNA
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(316)
<223> OTHER INFORMATION: Wherein N = A or C or G or T
<220> FEATURE:
<221> NAME/KEY: allele
<222> LOCATION: (73)..(73)
<223> OTHER INFORMATION: G to A
<220> FEATURE:
<221> NAME/KEY: allele
<222> LOCATION: (136)..(136)
<223> OTHER INFORMATION: A to G

<400> SEQUENCE: 219

```
gtccaaagtt ggagatgata ggttctctca caataataat gtattgtttt cctcttacac     60

cctcactagg cagtccactg ctgacccaac tgnnnnnnnn tgcactatat caatttctga    120

ctttatggag ataaaatagc tgtgatgtac ccagcttata ataaccctcc ttctacttag    180

agccacttgt tctctcctca gttttatttt actcctgaaa aaaaccctct tctcttttaa    240

actctattca taggtccttc acatcatttt aatcaaaaga tttcagggtc ttctataaca    300

acatttccca gtttca                                                    316
```

<210> SEQ ID NO 220
<211> LENGTH: 330
<212> TYPE: DNA
<213> ORGANISM: canine genomic DNA
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(330)

```
<223> OTHER INFORMATION: Wherein N = A or C or G or T
<220> FEATURE:
<221> NAME/KEY: allele
<222> LOCATION: (89)..(89)
<223> OTHER INFORMATION: C to T

<400> SEQUENCE: 220

aaagcccagc tgttgtctgg agccctgnnn nnnngaaaca ctggactttc caggccctcc      60

cttgaccttg actttcaagg gctctgtccg gatgcccttg ccttctcctg cctgnnnnnn     120

nnngggagca aaggaagctg gagctctggt tgttgcacaa cagaaagtcc tggctcctga     180

cactgagtga ttaaatgtga tttttctttt aagaaaaaag aagcctttta tcatactcct     240

agggctgtca gaaaccattc cggtagattt tcctaagtct tgtttttca gatgcgaaag      300

tggganncg tagctgtcct caccctatct                                       330


<210> SEQ ID NO 221
<211> LENGTH: 325
<212> TYPE: DNA
<213> ORGANISM: canine genomic DNA
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(325)
<223> OTHER INFORMATION: Wherein N = A or C or G or T
<220> FEATURE:
<221> NAME/KEY: allele
<222> LOCATION: (93)..(93)
<223> OTHER INFORMATION: C to T

<400> SEQUENCE: 221

cctgtccttt agaatcctca tcttgtacat gagagaggga tgaagacagg gaaggcagga      60

gggacggagg gagaaggaag tagctggcta ttcttctgaa ttagaatatg atannnnnnn     120

nnttttaaat cgaaaaatag gaaaaattca aaatctgaca attagcagag ggctttttgc     180

cctcagaata ttgcaaagaa tgaacaatca ttttataatt atgtcctttt tgtattttgt     240

atttttgtat ggaagttaac acttccatag taacatacat cttctagant tatgacctcc     300

tttccctctg gtgcttgaat gtgta                                           325


<210> SEQ ID NO 222
<211> LENGTH: 325
<212> TYPE: DNA
<213> ORGANISM: canine genomic DNA
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(325)
<223> OTHER INFORMATION: Wherein N = A or C or G or T
<220> FEATURE:
<221> NAME/KEY: allele
<222> LOCATION: (131)..(131)
<223> OTHER INFORMATION: Insert 2 “A”s
<220> FEATURE:
<221> NAME/KEY: allele
<222> LOCATION: (202)..(202)
<223> OTHER INFORMATION: C to T
<220> FEATURE:
<221> NAME/KEY: allele
<222> LOCATION: (242)..(242)
<223> OTHER INFORMATION: C to T

<400> SEQUENCE: 222

agtcatttat tgaagcaaag ggtgcaggga agggaaggag tagaaaataa aaatgaaaag      60

gaagattaag atcatattca aaaggccctt ataaaattca tttttggata aatctacaac     120

ggnnnnnnnn naccccaaat ttggatattt ggtctatttt cagtctctca tccatgtcaa     180

ttaacattag aagcaggaag ccctgtcctg ggactaatgg ctggctcaga gtcatgctac     240
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ttgacccgat gccctgtaac tctacaatca tgggcagggt gccaagcaag aacaagcact    300

ccacactcaa tccaggtgta cagag                                          325


<210> SEQ ID NO 223
<211> LENGTH: 315
<212> TYPE: DNA
<213> ORGANISM: canine genomic DNA
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(315)
<223> OTHER INFORMATION: Wherein N = A or C or G or T
<220> FEATURE:
<221> NAME/KEY: allele
<222> LOCATION: (50)..(50)
<223> OTHER INFORMATION: T to C
<220> FEATURE:
<221> NAME/KEY: allele
<222> LOCATION: (102)..(102)
<223> OTHER INFORMATION: Delete 8 Bases
<220> FEATURE:
<221> NAME/KEY: allele
<222> LOCATION: (130)..(130)
<223> OTHER INFORMATION: G to A

<400> SEQUENCE: 223

cgatatttag gaatgaagcc acattctttt catgacaaag catatgacct actctacaat     60

ctcctgaagc cagaatgctc ntacnctagt agtgaacaga gatctgaaga tctgaagaaa    120

ccaaacatag taaaagaaaa gacactgaga ggagagaagg ggcaagatgc agtgactctc    180

gcaatgcagt gacttaaggc accaaaccca tcagctagct atttaaatag ttggaaaata    240

agagtaaaag ccaagaaaca aaagataaga ttgttattaa agggcagana cnncgaagtg    300

cctatttgca tacca                                                     315


<210> SEQ ID NO 224
<211> LENGTH: 315
<212> TYPE: DNA
<213> ORGANISM: canine genomic DNA
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(315)
<223> OTHER INFORMATION: Wherein N = A or C or G or T
<220> FEATURE:
<221> NAME/KEY: allele
<222> LOCATION: (116)..(116)
<223> OTHER INFORMATION: C to T
<220> FEATURE:
<221> NAME/KEY: allele
<222> LOCATION: (282)..(282)
<223> OTHER INFORMATION: A to G

<400> SEQUENCE: 224

aaatatctgt ttctgaaata tctccctaaa aaactgtata tgtctgtatg catacaattc     60

acgtagtata cagctaccgt gaacgtttct tgcatgatgt cagccagtag ggannnnnnn    120

nnnngaccaa actatagctt ttgacccatg agcatcaggc tgctaaatcc ccgcaagggc    180

cttttacaac tttatcctgg gcagaagaat tttccttggt gtgtttctct cactggtgtg    240

tctctttcag ctacttgttt tgtgttctga taagcagtta gagctcgtaa tgacactatt    300

acgggctaga tctgc                                                     315


<210> SEQ ID NO 225
<211> LENGTH: 324
<212> TYPE: DNA
<213> ORGANISM: canine genomic DNA
<220> FEATURE:
```

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<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(324)
<223> OTHER INFORMATION: Wherein N = A or C or G or T
<220> FEATURE:
<221> NAME/KEY: allele
<222> LOCATION: (84)..(84)
<223> OTHER INFORMATION: Delete T
<220> FEATURE:
<221> NAME/KEY: allele
<222> LOCATION: (242)..(242)
<223> OTHER INFORMATION: G to A
<220> FEATURE:
<221> NAME/KEY: allele
<222> LOCATION: (243)..(243)
<223> OTHER INFORMATION: C to T

<400> SEQUENCE: 225

tttcctttgc ttctggtgct ggannnnnnc tttnnntggg aatttcatct cctgtttttta     60

agaaaaagaa agatcagggt gtttttcttg tatttgctat ttttcaagtg cctctaactc    120

aaaataacac tcgtaccaca gtgatgtatt ttggggnnnn nnnnnctgcc accctcagtg    180

tgtatatgta tttgtcaaaa gccagtgaat tatgcattta aaataggtac atttttattc    240

gatgtaagct aataccacaa tacaatttga tagaattttt aaaatagttt aaaaatagcc    300

cccaaaagcc agaagagtta gcaa                                            324


<210> SEQ ID NO 226
<211> LENGTH: 421
<212> TYPE: DNA
<213> ORGANISM: canine genomic DNA
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(421)
<223> OTHER INFORMATION: Wherein N = A or C or G or T
<220> FEATURE:
<221> NAME/KEY: allele
<222> LOCATION: (224)..(224)
<223> OTHER INFORMATION: T to C
<220> FEATURE:
<221> NAME/KEY: allele
<222> LOCATION: (246)..(246)
<223> OTHER INFORMATION: G to A
<220> FEATURE:
<221> NAME/KEY: allele
<222> LOCATION: (249)..(249)
<223> OTHER INFORMATION: Insert A
<220> FEATURE:
<221> NAME/KEY: allele
<222> LOCATION: (251)..(251)
<223> OTHER INFORMATION: Delete A
<220> FEATURE:
<221> NAME/KEY: allele
<222> LOCATION: (378)..(378)
<223> OTHER INFORMATION: A to C

<400> SEQUENCE: 226

ttggtttgat cacctatgga aggctgaaca aatccgggta ggattagatc gnnnnnnggg     60

agagaacaat tctccttgcc ctctttgggt ctctggctga ttctgaggat taaactgact    120

taagacaggg taacaggaga aaagtgtaga cacattattg aattntnnnn nnacatggga    180

ggccttcact tcacaaggga gtgaagaccc agggacatga ccaaagcagg aagattttaa    240

accttctgac aaagaaacaa tgagtttgtg aagaattgac aaggcacagg gatttgggtt    300

aggggtagta aatgctgaaa aattaaggtt tgtttataca gccttctcag ccctaaagcc    360

cctcttggtg ataaggctgt gtcccctcct tcagtacaag gggaagttgt atctcacatg    420

t                                                                     421
```

<210> SEQ ID NO 227
<211> LENGTH: 395
<212> TYPE: DNA
<213> ORGANISM: canine genomic DNA
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(395)
<223> OTHER INFORMATION: Wherein N = A or C or G or T
<220> FEATURE:
<221> NAME/KEY: allele
<222> LOCATION: (199)..(199)
<223> OTHER INFORMATION: A to C
<220> FEATURE:
<221> NAME/KEY: allele
<222> LOCATION: (224)..(224)
<223> OTHER INFORMATION: G to A

<400> SEQUENCE: 227

acacataact gaagcacacc agcaatatga cagtannnnn nnnnnnnnag ggaaaaaatg 60

tatgaacagg atgttgaggt tttactttta cttgttgcat tcccttaaaa aataataacc 120

attatggcaa aaatatggac ttcattttag tggtatctgt gtattcatat tattttgcac 180

ttttctaagg tttgcattat ctcacaattg aaaagaaaaa cacgagctaa gtaaaatgtt 240

aacatatatt attgctacat ttaaaagnnn acaggaagtt taaaaacaaa tgcacccatt 300

attcattaat ttttcactgc tattaagttt aatcaactct tagttttctc tctcagncct 360

aagtagatta tttcaaggaa gtcatgctca atctt 395

<210> SEQ ID NO 228
<211> LENGTH: 439
<212> TYPE: DNA
<213> ORGANISM: canine genomic DNA
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(439)
<223> OTHER INFORMATION: Wherein N = A or C or G or T
<220> FEATURE:
<221> NAME/KEY: allele
<222> LOCATION: (249)..(249)
<223> OTHER INFORMATION: C to T
<220> FEATURE:
<221> NAME/KEY: allele
<222> LOCATION: (250)..(250)
<223> OTHER INFORMATION: C to T
<220> FEATURE:
<221> NAME/KEY: allele
<222> LOCATION: (254)..(254)
<223> OTHER INFORMATION: G to A
<220> FEATURE:
<221> NAME/KEY: allele
<222> LOCATION: (312)..(312)
<223> OTHER INFORMATION: A to G

<400> SEQUENCE: 228

taggtgcatc ccattctcag ggggccattg gggccacagc agccttcccn nnnngcctnn 60

nnnnnnnnnn gccgtggtgt ttcctctgcn nnnnnccagg ctggggcggc aggcaggggt 120

ggggcctccc ttggagaaan nnnagctgcc tctgtcctgg gctgggctga gctgggagag 180

gccacgccag gtccttctgc ccagatgcca cctcctcccc gctcctcttg gcctctccag 240

ccgcaggccc ggcgcctccc anngagtggg acctgctcct gtgagtcagn nnnnngacnn 300

nnnnngtgca cagatnnact atannnngta tnnnactggt catgtgttta tttnnnngag 360

tatcnnnnnn nnncnnacaa gcaattaatg cgcgnaaccc tngatnncat nnattnnann 420

gctcaaggcg aggcaaatt 439

<210> SEQ ID NO 229

```
<211> LENGTH: 342
<212> TYPE: DNA
<213> ORGANISM: canine genomic DNA
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(342)
<223> OTHER INFORMATION: Wherein N = A or C or G or T
<220> FEATURE:
<221> NAME/KEY: allele
<222> LOCATION: (181)..(181)
<223> OTHER INFORMATION: C to T
<220> FEATURE:
<221> NAME/KEY: allele
<222> LOCATION: (224)..(224)
<223> OTHER INFORMATION: Delete 2 Bases

<400> SEQUENCE: 229

ccaatgatct tgcacagtta tgttacnnnn nnnnncttta aaaaacatat aactgagtac     60

ggtggttccn nnnnnacatc ctttaattgc tccccagcat ctaaaggaca atgcccnnnc    120

tcctgaacac ggatacggat ccccacctca nngtcctgtc catttctctc gtatcacttg    180

ccatccacca actccagctc atttactgcc atggaaacaa agagagccat caaatttgag    240

atgttttatg ttacnnnnnn ntttagctga aacatctttt ttttgtctag ttatagtcct    300

aatcttcttt cannnnnntc cactccaata ccacctctac ca                       342


<210> SEQ ID NO 230
<211> LENGTH: 357
<212> TYPE: DNA
<213> ORGANISM: canine genomic DNA
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(357)
<223> OTHER INFORMATION: Wherein N = A or C or G or T
<220> FEATURE:
<221> NAME/KEY: allele
<222> LOCATION: (261)..(261)
<223> OTHER INFORMATION: A to C
<220> FEATURE:
<221> NAME/KEY: allele
<222> LOCATION: (264)..(264)
<223> OTHER INFORMATION: T to C

<400> SEQUENCE: 230

caaatgttaa atggacatct gcnnnnnnnn nnnctgcacn nggctannnn nngnnggnnn     60

gaaannnnct ttgtcttcat gnnnttggnn nnnnntcann nnnngagcnn nnncgtgcca    120

nnnnnnnnnn nnngtgaata atttaatgtc tgaatcagac atgattctga acttctttgt    180

tttacagatg aggaaattga acttatctgt gtctgcttca accccaggat ttccttattc    240

tttgattcaa aacttgacct aaataatcct gtagaannat agagaaaagg gtcgtcgaaa    300

tgctcgtgat acggaaatga gagtctgatt gtcatgttct ttctcaggcc tctatca       357


<210> SEQ ID NO 231
<211> LENGTH: 317
<212> TYPE: DNA
<213> ORGANISM: canine genomic DNA
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(317)
<223> OTHER INFORMATION: Wherein N = A or C or G or T
<220> FEATURE:
<221> NAME/KEY: allele
<222> LOCATION: (112)..(112)
<223> OTHER INFORMATION: A to G
<220> FEATURE:
<221> NAME/KEY: allele
<222> LOCATION: (168)..(168)
<223> OTHER INFORMATION: A to G
```

```
<400> SEQUENCE: 231

ggtaaaccag aagttcccca ggtgaaatgg cttttcctcc attaccctcc ccagtcacac     60

aaccagagga aagtgggctg aaactgagca ttcagngata gaggatgggg tgctgagtgn    120

nctnnnnnna cggaggtccc ataggtccaa gggctgaacc caggtacagg gggcgtgaga    180

aaggggcctg agaggtctac gggagactgg aaactctggg ggcgcagaag cgggggaaga    240

accctggcga tcacgcctgc gggctggcaa agggacggaa aacccaanng gggagaganc    300

ttgagccttc gcaacag                                                   317


<210> SEQ ID NO 232
<211> LENGTH: 325
<212> TYPE: DNA
<213> ORGANISM: canine genomic DNA
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(325)
<223> OTHER INFORMATION: Wherein N = A or C or G or T
<220> FEATURE:
<221> NAME/KEY: allele
<222> LOCATION: (121)..(121)
<223> OTHER INFORMATION: T to C
<220> FEATURE:
<221> NAME/KEY: allele
<222> LOCATION: (196)..(196)
<223> OTHER INFORMATION: G to A

<400> SEQUENCE: 232

atttacatgg cagtgtgttc tggttatcta cttctgtata acaaatgacc ttaaaattta     60

gtggcttaaa acagtaattc atcattataa ttcacagttc ttngngttga ctgggccctc    120

ttgggtagtt cttgcttgca atctctcatg gagttgtagt caggtacagg ctgggagggg    180

ctgcaattct ctggaggttt tagtgagccc agcatccaaa atggtgccct catatggctg    240

gtgattgata gtggctgctg tctgggagct cagctggaac tatcaaatgg actgtcctca    300

tgtggctcat gttatgtggg ctttt                                          325


<210> SEQ ID NO 233
<211> LENGTH: 250
<212> TYPE: DNA
<213> ORGANISM: canine genomic DNA
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(250)
<223> OTHER INFORMATION: Wherein N = A or C or G or T
<220> FEATURE:
<221> NAME/KEY: allele
<222> LOCATION: (67)..(67)
<223> OTHER INFORMATION: A to G
<220> FEATURE:
<221> NAME/KEY: allele
<222> LOCATION: (71)..(71)
<223> OTHER INFORMATION: A to C
<220> FEATURE:
<221> NAME/KEY: allele
<222> LOCATION: (165)..(165)
<223> OTHER INFORMATION: G to A
<220> FEATURE:
<221> NAME/KEY: allele
<222> LOCATION: (221)..(221)
<223> OTHER INFORMATION: C to A

<400> SEQUENCE: 233

attccatttt aggtctgcat aaaggcaaca atgttgtcaa aagtttagnn nnnnnnnnnn     60

nntaaaacca atgaatcacg gaagtactaa ttagtaaaag ttgatcatgc acacagagtt    120
```

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ctaaataagt aaattaatgg agagacataa tacacttatg gattgtagaa tttaagatgt 180

tagtcatctc caaatttttc aaaagatata ataaaatttc catcaacttc ttggcaggca 240

ctctctaaaa 250

<210> SEQ ID NO 234
<211> LENGTH: 245
<212> TYPE: DNA
<213> ORGANISM: canine genomic DNA
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(245)
<223> OTHER INFORMATION: Wherein N = A or C or G or T
<220> FEATURE:
<221> NAME/KEY: allele
<222> LOCATION: (97)..(97)
<223> OTHER INFORMATION: A to G
<220> FEATURE:
<221> NAME/KEY: allele
<222> LOCATION: (224)..(224)
<223> OTHER INFORMATION: Insert T

<400> SEQUENCE: 234

aaactctcct atttcacatt gaccattttt ctatgaatga aggaataata tttttataac 60

cctgttcccc tccctctgaa tgttttatga aaagaannnn nnnnnnnnnn nnaaaattca 120

agaagtgaaa ggaaaattga attttccttc ctcagagaag aagtttaaat caatcatcct 180

tgagaaaaat ctaaatggtc caaattatct ggagccattt tttgtaagat tggatttgcc 240

agttc 245

<210> SEQ ID NO 235
<211> LENGTH: 297
<212> TYPE: DNA
<213> ORGANISM: canine genomic DNA
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(297)
<223> OTHER INFORMATION: Wherein N = A or C or G or T
<220> FEATURE:
<221> NAME/KEY: allele
<222> LOCATION: (67)..(67)
<223> OTHER INFORMATION: A to G
<220> FEATURE:
<221> NAME/KEY: allele
<222> LOCATION: (73)..(73)
<223> OTHER INFORMATION: A to C
<220> FEATURE:
<221> NAME/KEY: allele
<222> LOCATION: (100)..(100)
<223> OTHER INFORMATION: T to C
<220> FEATURE:
<221> NAME/KEY: allele
<222> LOCATION: (108)..(108)
<223> OTHER INFORMATION: C to T
<220> FEATURE:
<221> NAME/KEY: allele
<222> LOCATION: (127)..(127)
<223> OTHER INFORMATION: T to A
<220> FEATURE:
<221> NAME/KEY: allele
<222> LOCATION: (147)..(147)
<223> OTHER INFORMATION: T to G
<220> FEATURE:
<221> NAME/KEY: allele
<222> LOCATION: (186)..(186)
<223> OTHER INFORMATION: A to G

<400> SEQUENCE: 235

acaaaagaac cctcctgtct ctgtaaccan nnncaagaag gacagtaagg ctgggtcctt 60

atgtaaacga gcctgagtac atatctaagt gctctcatgc ttaagggcag aagttccctn 120 nnnnnnnnnn aaagtaaagg cagagataat ttcatctctg aggggaaagg gtaaaataat 180

gcttcagcaa tcactcaaat aggggcaggg agcatctgaa aaggattaat tcacccgtgc 240

aatagatatc tagctaaatc tctactatga gtattttctc tttctttcct ttaagat 297

<210> SEQ ID NO 236
<211> LENGTH: 338
<212> TYPE: DNA
<213> ORGANISM: canine genomic DNA
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(338)
<223> OTHER INFORMATION: Wherein N = A or C or G or T
<220> FEATURE:
<221> NAME/KEY: allele
<222> LOCATION: (100)..(100)
<223> OTHER INFORMATION: C to A
<220> FEATURE:
<221> NAME/KEY: allele
<222> LOCATION: (273)..(273)
<223> OTHER INFORMATION: A to G

<400> SEQUENCE: 236

cttttggctt tctctgaatt tgcataaact ccagtaatct tttttttccc cctgggttga 60

taatagtgtt tgtgttaaaa tcacaccttc ttttcatttc ttgcatgcat ataggctttt 120

ctcctgtttg tggacacaag tgcttttatc tcactctgca atcagtcaca accccgggtg 180

gaggcaggga acatttgcta caatatttcc tatataaaca gtttcactgt aaaaggaaca 240

atatggctct aattttgatg tatgatcagt ttagaaatat gcaaacacat ttgaatatac 300

atcctgtaca tgacaacagc aatgtgaaat tggataca 338

<210> SEQ ID NO 237
<211> LENGTH: 304
<212> TYPE: DNA
<213> ORGANISM: canine genomic DNA
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(304)
<223> OTHER INFORMATION: Wherein N = A or C or G or T
<220> FEATURE:
<221> NAME/KEY: allele
<222> LOCATION: (131)..(131)
<223> OTHER INFORMATION: T to C

<400> SEQUENCE: 237

taagttccac ctgtattgca tcagattgtt gttgaaaaac actgccaata attgcttttn 60

nnnttgccag gctagttggg agtggaaagg gggctggaac tatggaatca gacctaacta 120

tgatctactt cggtccctaa atccctgagt aacaacagca ggcagagcag tgaacctctc 180

tgatctacag tttctgcctc tgcaaaatgg gggtcattct tcccacctca tggaacaccc 240

tgtggtcttc agcctatttc tagcccgggg taggtgctca gagaagacaa gtgatgatgg 300

gttt 304

<210> SEQ ID NO 238
<211> LENGTH: 412
<212> TYPE: DNA
<213> ORGANISM: canine genomic DNA
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(412)
<223> OTHER INFORMATION: Wherein N = A or C or G or T
<220> FEATURE:
<221> NAME/KEY: allele
<222> LOCATION: (55)..(55)

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<223> OTHER INFORMATION: Delete T
<220> FEATURE:
<221> NAME/KEY: allele
<222> LOCATION: (160)..(160)
<223> OTHER INFORMATION: A to T
<220> FEATURE:
<221> NAME/KEY: allele
<222> LOCATION: (197)..(197)
<223> OTHER INFORMATION: C to T
<220> FEATURE:
<221> NAME/KEY: allele
<222> LOCATION: (290)..(290)
<223> OTHER INFORMATION: T to C

<400> SEQUENCE: 238

gatcttttgt gctcagtgag agaantnnnn nttcaannnn nnnnnnnngn atccaacaaa     60

tacaaaaagc nnnnnaacat aaaatagaca tttataagtc acttgtatgt atattggctt    120

tttgtaaatt aaatcatgtt ttatataaca ttagaaccct gttgggtaag gccccctgaa    180

gtaaatggtt tgtaatagaa ataaattgcc ctaccacttg tgatgagcat agcataacaa    240

ccaaagttgt tgaatcactt tgttgtacac ctgaaactaa tgtaacattg tgtgtcaact    300

atactaaaaa ataataataa ataagttttt atttttaata actgctaaaa taaattaaaa    360

atgagtagtg atcctcgttt cagnaatacc tgaaacattt atctgcttat ga            412


<210> SEQ ID NO 239
<211> LENGTH: 300
<212> TYPE: DNA
<213> ORGANISM: canine genomic DNA
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(300)
<223> OTHER INFORMATION: Wherein N = A or C or G or T
<220> FEATURE:
<221> NAME/KEY: allele
<222> LOCATION: (93)..(93)
<223> OTHER INFORMATION: A to G

<400> SEQUENCE: 239

ccttatccta ccacagcttc agccatgtct ccagggcctg tgggatccta gagcactcca     60

tcaaggaagc agngtgaggt gaggggggag ctacannnnn ggcggattga cttgtatctc    120

cacnnnnnnn ttcctgtcac attttgatga tctgtcctca ggtttatgac aaatgcttat    180

tacatggtgt atggagacca gtatacagaa acactcttgt ttcctgtaac tcattctttt    240

tatttttgaa ttcctacttg atactcctgt ctaaaatgag ccctaaatat cacaaactca    300


<210> SEQ ID NO 240
<211> LENGTH: 300
<212> TYPE: DNA
<213> ORGANISM: canine genomic DNA
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(300)
<223> OTHER INFORMATION: Wherein N = A or C or G or T
<220> FEATURE:
<221> NAME/KEY: allele
<222> LOCATION: (136)..(136)
<223> OTHER INFORMATION: C to T
<220> FEATURE:
<221> NAME/KEY: allele
<222> LOCATION: (175)..(175)
<223> OTHER INFORMATION: C to T
<220> FEATURE:
<221> NAME/KEY: allele
<222> LOCATION: (191)..(191)
<223> OTHER INFORMATION: G to C

<400> SEQUENCE: 240
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acccacagaa tccacaagca taattattgt ttaaagcctt tgtatttgga gccgattgtt 60

acaacagcaa ttattttttt aaaaattgta tttatttatt catgagagac acagaannnn 120

nnnnnnnnnn nnngacacag tgnnnnnnnn gaagcaggct ctctgtgggg agcccgatgt 180

gggactcgat gcctgggccc caatcacact ctgagccaaa ggcaaatact cacccactga 240

cccactcagg tgcccctata ccagcaatta gaacactagg cttgtcctta cacctatttt 300

<210> SEQ ID NO 241
<211> LENGTH: 304
<212> TYPE: DNA
<213> ORGANISM: canine genomic DNA
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(304)
<223> OTHER INFORMATION: Wherein N = A or C or G or T
<220> FEATURE:
<221> NAME/KEY: allele
<222> LOCATION: (263)..(263)
<223> OTHER INFORMATION: C to T
<220> FEATURE:
<221> NAME/KEY: allele
<222> LOCATION: (266)..(266)
<223> OTHER INFORMATION: T to C

<400> SEQUENCE: 241

catctgctgg cacaacttcc tcttgctctg gggaggtcag ttttttctgt tttagtcaaa 60

ctcttcaact gattagatga ggtccacctg cattatgaag ggatatctgc tttannnnnn 120

nnnnnactga tttgaattcc aaaacacctt cacaaaaaac attccaaatg ttgtttgagc 180

aaatatctgg gcaccatggt ccagtcaggt tgacacaaaa ttaacagtca caccactatg 240

agtcctgtgt atccatatta tttctttaag ctacgtttat gaaagtgaaa tctaatagga 300

tgca 304

<210> SEQ ID NO 242
<211> LENGTH: 342
<212> TYPE: DNA
<213> ORGANISM: canine genomic DNA
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(342)
<223> OTHER INFORMATION: Wherein N = A or C or G or T
<220> FEATURE:
<221> NAME/KEY: allele
<222> LOCATION: (47)..(47)
<223> OTHER INFORMATION: G to A
<220> FEATURE:
<221> NAME/KEY: allele
<222> LOCATION: (133)..(133)
<223> OTHER INFORMATION: C to T
<220> FEATURE:
<221> NAME/KEY: allele
<222> LOCATION: (173)..(173)
<223> OTHER INFORMATION: G to A
<220> FEATURE:
<221> NAME/KEY: allele
<222> LOCATION: (210)..(210)
<223> OTHER INFORMATION: G to A
<220> FEATURE:
<221> NAME/KEY: allele
<222> LOCATION: (302)..(302)
<223> OTHER INFORMATION: C to T
<220> FEATURE:
<221> NAME/KEY: allele
<222> LOCATION: (319)..(319)
<223> OTHER INFORMATION: C to A

<400> SEQUENCE: 242

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tattgagccc aactgtatac ccgagcctgc gcttggtgct gagggggtag tggtggcaac 60

actgagcctt taccatccac tccaccgcac tcacagtgag atgaggatca gcacataaac 120

ccgggattcc agcgtgggac acgctgagac agaaggcaac ctgaggcaga cgggggggtta 180

gggtgggtgg gacaggcagc catgannnnn nggacnnnnn tcannnnnna tgannannag 240

acacagatcn nnngttngan nagagagggt cattcnnnnn ggcaggagca gcgcgtgcaa 300

annngccatg atgcccagnn tgctgtgtca tgggaaccag at 342

<210> SEQ ID NO 243
<211> LENGTH: 331
<212> TYPE: DNA
<213> ORGANISM: canine genomic DNA
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(331)
<223> OTHER INFORMATION: Wherein N = A or C or G or T
<220> FEATURE:
<221> NAME/KEY: allele
<222> LOCATION: (54)..(54)
<223> OTHER INFORMATION: Insert A

<400> SEQUENCE: 243

tgacagtaag ttgtgcaggt tccttttctt tccccccaaa tgagtctttt actatttttt 60

ttctaannnn agctaccttc agnnnnnnnn nnnnnncnaa gtcaannnnn acacatccct 120

tgacacagac acctaaatct ctgtaatttt tgagcaagaa cttgatttgc tatatgccat 180

aagctaaatg gatagtttgg ggcacacatt tgtctggaga caaagccttg ctctaaacaa 240

cagtttaaaa tgtttcagtg agcacctatt gaaagtgata tattatgcaa gcaatttctt 300

tgtagttatg cgtagaaaca gctcagctac t 331

<210> SEQ ID NO 244
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 244

gcttttggac aactttggat ag 22

<210> SEQ ID NO 245
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 245

gaattccaaa tgtcctgctt ag 22

<210> SEQ ID NO 246
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 246

aagcatactt ccctgaaatg ag 22

<210> SEQ ID NO 247
<211> LENGTH: 22

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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 247

agtcaaatcg ttcattggat tc                                              22


<210> SEQ ID NO 248
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 248

aaaaggtggc acatatgaaa ag                                              22


<210> SEQ ID NO 249
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 249

ggggtttcta ttccattttc ac                                              22


<210> SEQ ID NO 250
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 250

acctcatgta tgtcttgttc cc                                              22


<210> SEQ ID NO 251
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 251

ctctgctagg agaaaaggag ag                                              22


<210> SEQ ID NO 252
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 252

caaatggttc aagaggagat tc                                              22


<210> SEQ ID NO 253
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 253
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aaagtaaaat caggtattct cctcc                                             25


<210> SEQ ID NO 254
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 254

caccctcaag aagttaaagc ac                                                22


<210> SEQ ID NO 255
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 255

taggggacac agtttctaaa gg                                                22


<210> SEQ ID NO 256
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 256

tctcaaactg ttgaagacca ac                                                22


<210> SEQ ID NO 257
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 257

catgtgaccc ttcctatgag ac                                                22


<210> SEQ ID NO 258
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 258

ggaagacccc aactctatta ttg                                               23


<210> SEQ ID NO 259
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 259

agtcttttgg tcctaaacat gg                                                22


<210> SEQ ID NO 260
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 260

agacacatgc attttcccag                                                    20


<210> SEQ ID NO 261
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 261

gtccaaagtt ggagatgata gg                                                 22


<210> SEQ ID NO 262
<211> LENGTH: 19
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 262

aaagcccagc tgttgtctg                                                     19


<210> SEQ ID NO 263
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 263

cctgtccttt agaatcctca tc                                                 22


<210> SEQ ID NO 264
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 264

agtcatttat tgaagcaaag gg                                                 22


<210> SEQ ID NO 265
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 265

cgatatttag gaatgaagcc ac                                                 22


<210> SEQ ID NO 266
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 266

aaatatctgt ttctgaaata tctccc                                             26
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<210> SEQ ID NO 267
<211> LENGTH: 19
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 267

tttcctttgc ttctggtgc                                                19


<210> SEQ ID NO 268
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 268

ttggtttgat cacctatgga ag                                            22


<210> SEQ ID NO 269
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 269

acacataact gaagcacacc ag                                            22


<210> SEQ ID NO 270
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 270

taggtgcatc ccattctcag                                               20


<210> SEQ ID NO 271
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide Primer

<400> SEQUENCE: 271

ccaatgatct tgcacagtta tg                                            22


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The embodiments of the invention in which an exclusive property or privilege is claimed are defined as follows:

1. A method for determining the contributions of canid populations to a canid genome, comprising:

(a) genotyping a sample obtained from a test canid to determine the identity of one or both alleles present in the test canid genome for each of a set of markers, wherein the set of markers is indicative of the contributions of canid populations to the genome of the test canid;

(b) using a specifically programmed computer comprising an algorithm to compare the identity of one or both alleles for each of the set of markers determined to be present in the test canid genome to a database comprising a plurality of canid population profiles, wherein each canid population profile comprises genotype information for the set of markers in the canid population; and

(c) determining the contributions of canid populations to the test canid genome.

2. The method of claim **1**, wherein the set of markers comprises at least about five markers.

3. The method of claim **1**, wherein the set of markers comprises microsatellite markers.

4. The method of claim **3**, wherein the micro satellite markers comprise at least 5 of the micro satellite markers set forth in Table 1.

5. The method of claim **1**, wherein the set of markers comprises single nucleotide polymorphisms (SNPs).

6. The method of claim **5**, wherein the SNP markers comprise at least 5 of the SNP markers set forth in Table 2.

7. The method of claim **1**, wherein the set of markers comprises one or more population-specific markers.

8. The method of claim **7**, wherein the one or more population-specific markers comprise one or more SNP markers.

9. The method of claim **8**, wherein the one or more population specific SNP markers are selected from the group consisting of position 82 of SEQ ID NO: 202, position 57 of SEQ ID NO: 205, position 88 of SEQ ID NO: 211, position 76 of SEQ ID NO: 215, position 112 of SEQ ID NO: 218, position 50 of SEQ ID NO: 223, position 130 of SEQ ID NO: 223, position 246 of SEQ ID NO: 226, position 224 of SEQ ID NO: 227, position 181 of SEQ ID NO: 229, position 168 of SEQ ID NO: 231, position 196 of SEQ ID NO: 232, position 71 of SEQ ID NO: 233, and position 93 of SEQ ID NO: 239.

10. The method of claim **1**, wherein the genotype information in each canid population profile comprises identities of one or both alleles of each of the set of markers.

11. The method of claim **1**, wherein the genotype information in each canid population profile comprises allele frequencies for at least one allele of each of the set of markers.

12. The method of claim **1**, wherein the database of canid population profiles comprises between about five and about 500 canid population profiles.

13. The method of claim **1**, wherein the database of canid populations profiles comprise profiles for at least about five American Kennel Club registered breeds.

14. The method of claim **1**, wherein the set of markers comprises fewer than about 1500 SNP markers and wherein the method determines the contributions of at least 87 canid populations to the test canid genome.

15. The method of claim **1**, wherein the set of markers comprises fewer than about 200 SNP markers and wherein the method determines the contributions of at least 87 canid populations to the test canid genome.

16. The method of claim **1**, wherein step (a) comprises amplifying genomic DNA of the test canid using primers specific for each of the set of markers and determining the size of the amplification product.

17. The method of claim **1**, wherein the algorithm according to step (b) comprises a genotype clustering program.

18. The method of claim **1**, wherein the algorithm according to step (b) comprises an assignment algorithm.

19. The method of claim **1**, wherein applying the algorithm according to step (b) comprises determining the probability that a specific canid population contributed to the genome of the test canid by determining the conditional probability that the alleles in the test canid genome would occur in the specific canid population divided by the sum of conditional probabilities that the alleles in the test canid genome would occur in each canid population in the database.

20. The method of claim **1**, wherein step (b) comprises discriminating between the contributions of two or more genetically related canid populations to the test canid genome by comparing the alleles in the test canid genome to a database comprising profiles of the two or more genetically related canid populations.

21. The method of claim **20**, wherein the two or more genetically related canid populations comprise Belgian Sheep Dog and Belgian Tervuren.

22. The method of claim **20**, wherein the two or more genetically related canid populations comprise Collie and Shetland Sheep Dog.

23. The method of claim **20**, wherein the two or more genetically related canid populations comprise Whippet and Greyhound.

24. The method of claim **20**, wherein the two or more genetically related canid populations comprise Siberian Husky and Alaskan Malamute.

25. The method of claim **20**, wherein the two or more genetically related canid populations comprise Mastiff and Bullmastiff.

26. The method of claim **20**, wherein the two or more genetically related canid populations comprise Greater Swiss Mountain Dog and Bernese Mountain Dog.

27. The method of claim **20**, wherein the two or more genetically related canid populations comprise West Highland White Terrier and Cairn Terrier.

28. The method of claim **20**, wherein the two or more genetically related canid populations comprise Lhasa Apso, Shih Tzu, and Pekinese.

29. The method of claim **1** further comprising the step of providing a document displaying the contributions of one or more canid populations to the genome of the test canid genome.

30. The method of claim **29**, wherein the document provides additional information regarding the one or more canid populations that contributed to the genome of the test canid or the test canid.

31. The method of claim **30**, wherein the additional information is health-related information.

32. The method of claim **30**, wherein the additional information is insurance information.

33. The method of claim **29**, wherein the document provides a certification of the contributions of one or more canid populations to the genome of the test canid genome.

34. The method of claim **29**, wherein the document provides a representation of the one or more canid populations that contributed to the genome of the test canid.

35. A method for defining one or more canid populations, comprising:

(a) performing a genotyping assay on a set of canid genomes, to determine the identity of one or both alleles for each of a set of markers, wherein the set of markers is indicative of the contributions of canid populations to the genomes of each member of the set of canids; and

(b) applying a computer-implemented statistical model to define one or more distinct canid populations, wherein one or more distinct canid populations are characterized by a set of allele frequencies for each marker in the set of markers.

36. A computer readable medium comprising stored thereon:

(a) a data structure stored thereon for use in distinguishing canid populations, the data structure comprising:

(i) a marker field, which is capable of storing the name of a marker or of an allele of the marker; and

(ii) a genotype information field, which is capable of storing genotype information for the marker in a canid population, wherein a record comprises an instantiation of the marker field and an instantiation of the genotype information field and a set of records represents a canid population profile; and

(b) computer-executable instructions for implementing a method for determining the contributions of canid populations to a canid genome, comprising:

(i) obtaining the identity of one or both alleles in a test canid genome for each of a set of markers; and

(ii) determining the contributions of canid populations to the test canid genome by comparing the alleles in the test canid genome to a database comprising canid population profiles, wherein each canid population profile comprises genotype information for the set of markers in the canid population.

37. A computer-readable medium comprising a data structure stored thereon for use in distinguishing canid populations, the data structure comprising:

(a) a marker field, which is capable of storing the name of a marker or of an allele of the marker; and

(b) a genotype information field, which is capable of storing genotype information for the marker in a canid population, wherein a record comprises an instantiation of the marker field and an instantiation of the genotype information field and a set of records represents a canid population profile, wherein the marker field comprises a set of markers indicative of the contributions of canid populations to the genome of a test canid.

38. The computer readable medium of claim **36** wherein the marker field comprises a set of markers indicative of the contributions of canid populations to the genome of a test canid.

39. A method for determining the contributions of canid populations to a canid genome, comprising performing a genotyping assay on a sample obtained from a test canid to determine the identity of one or both alleles present in the test canid genome for each of a set of markers, wherein the set of markers is indicative of the contribution of canid populations to the genome of the test canid.

40. The method of claim **39**, wherein the set of markers comprises at least five markers.

41. The method of claim **39**, wherein the set of markers comprises microsatellite markers.

42. The method of claim **39**, wherein the set of markers comprises single nucleotide polymorphisms (SNPs).

43. The method of claim **39**, wherein the set of markers comprises one or more population-specific markers.

44. The method of claim **43**, wherein the population-specific markers are SNP markers.

* * * * *

UNITED STATES PATENT AND TRADEMARK OFFICE

CERTIFICATE OF CORRECTION

PATENT NO. : 7,729,863 C1
APPLICATION NO. : 95/000621
DATED : September 25, 2012
INVENTOR(S) : Elaine Ostrander et al.

Page 1 of 1

It is certified that error appears in the above-identified patent and that said Letters Patent is hereby corrected as shown below:

Title page, item “(73) Assignees:” on the cover page of the Reexamination Certificate reading:

“The United States of America as represented by the National Institutes of Health (NIH), Washington, DC (US); The United States of America as represented by the Department of Health and Human Services (DHHS), Washington, DC (US)” should read --Fred Hutchinson Cancer Research Center, Seattle, Washington (US)--

Signed and Sealed this
First Day of January, 2013

David J. Kappos

David J. Kappos
Director of the United States Patent and Trademark Office

UNITED STATES PATENT AND TRADEMARK OFFICE

CERTIFICATE OF CORRECTION

PATENT NO. : 7,729,863 B2
APPLICATION NO. : 10/536369
DATED : June 1, 2010
INVENTOR(S) : E. Ostrander et al.

Page 1 of 1

It is certified that error appears in the above-identified patent and that said Letters Patent is hereby corrected as shown below:

Column	Lines	Error
1	13-15	Delete the paragraph “The U.S. Government has a paid-up license in this invention and the right in limited circumstances to require the patent owner to license others on reasonable terms as provided for by the terms of HG300035 awarded by the National Institutes of Health.” and insert --This invention was made with government support under grant number HG000035 awarded by the National Institutes of Health. The government has certain rights in the invention.--

Signed and Sealed this
Twentieth Day of June, 2017

Joseph Matal

Joseph Matal
Performing the Functions and Duties of the
Under Secretary of Commerce for Intellectual Property and
Director of the United States Patent and Trademark Office

US007729863C1

(12) INTER PARTES REEXAMINATION CERTIFICATE (0458th)

United States Patent

Ostrander et al.

(10) **Number: US 7,729,863 C1**

(45) **Certificate Issued: Sep. 25, 2012**

---

(54) **METHODS AND MATERIALS FOR CANINE BREED IDENTIFICATION**

(75) Inventors: **Elaine Ostrander**, Seattle, WA (US); **Leonid Kruglyak**, Seattle, WA (US); **Heidi G Parker**, Seattle, WA (US); **Lisa V Kim**, Sammamish, WA (US); **Matthew Stephens**, Seattle, WA (US); **Tiffany B Malek**, Seattle, WA (US); **Nathan B Sutter**, Seattle, WA (US); **Scott Carlson**, Seattle, WA (US)

(73) Assignees: **The United States of America as represented by the National Institutes of Health (NIH)**, Washington, DC (US); **The United States of America as represented by the Department of Health and Human Services (DHHS)**, Washington, DC (US)

Reexamination Request:

No. 95/000,621, Apr. 28, 2011

Reexamination Certificate for:

Patent No.: **7,729,863**
Issued: **Jun. 1, 2010**
Appl. No.: **10/536,369**
Filed: **Feb. 1, 2006**

(22) PCT Filed: **Dec. 15, 2004**

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See application file for complete search history.

(56) **References Cited**

To view the complete listing of prior art documents cited during the proceeding for Reexamination Control Number 95/000,621, please refer to the USPTO's public Patent Application Information Retrieval (PAIR) system under the Display References tab.

Primary Examiner—Shri Ponnaluri

(57) **ABSTRACT**

In one aspect, the invention provides methods for determining the contributions of canid populations to a canid genome. The methods comprise the steps of: (a) obtaining the identity of one or both alleles in a test canid genome for each of a set of markers; and (b) determining the contributions of canid populations to the test canid genome by comparing the alleles in the test canid genome to a database comprising canid population profiles, wherein each canid population profile comprises genotype information for the set of markers in the canid populations.

INTER PARTES REEXAMINATION CERTIFICATE ISSUED UNDER 35 U.S.C. 316

THE PATENT IS HEREBY AMENDED AS INDICATED BELOW.

Matter enclosed in heavy brackets [ ] appeared in the patent, but has been deleted and is no longer a part of the patent; matter printed in italics indicates additions made to the patent.

AS A RESULT OF REEXAMINATION, IT HAS BEEN DETERMINED THAT:

Claims **1**, **5**, **7**, **8**, **29** and **30** are cancelled.

Claims **2**-**4**, **10**-**13**, **16**-**28**, **31** and **33**-**39** are determined to be patentable as amended.

Claims **40**-**44**, dependent on an amended claim, are determined to be patentable.

New claims **45**-**49** are added and determined to be patentable.

Claims **6**, **9**, **14**, **15** and **32** were not reexamined.

2. The method of claim [**1**] *13*, wherein the set of markers comprises at least about five markers.

3. The method of claim [**1**] *13*, wherein the set of markers comprises microsatellite markers.

4. [The method of claim **3**, wherein the] *A method for determining the contributions of canid populations to a canid genome, comprising:*

(*a*) *genotyping a sample obtained from a test canid to determine the identity of one or both alleles present in the test canid genome for each of a set of markers, wherein the set of markers is indicative of the contributions of canid populations to the genome of the test canid and wherein the set of markers comprises* microsatellite markers *that* comprise at least 5 of the micro satellite markers set forth in Table 1*;*

(*b*) *using a specifically programmed computer comprising an algorithm to compare the identity of one or both alleles for each of the set of markers determined to be present in the test canid genome to a database comprising a plurality of canid population profiles, wherein each canid population profile comprises genotype information for the set of markers in the canid population; and,*

(*c*) *determining the contributions of canid populations to the test canid genome.*

10. The method of claim [**1**] *13*, wherein the genotype information in each canid population profile comprises identities of one or both alleles of each of the set of markers.

11. The method of claim [**1**] *13*, wherein the genotype information in each canid population profile comprises allele frequencies for at least one allele of each of the set of markers.

12. [The method of claim **1**,] *A method for determining the contributions of canid populations to a canid genome, comprising:*

(*a*) *genotyping a sample obtained from a test canid to determine the identity of one or both alleles present in the test canid genome for each of a set of markers, wherein the set of markers is indicative of the contributions of canid populations to the genome of the test canid;*

(*b*) *using a specifically programmed computer comprising an algorithm to compare the identity of one or both alleles for each of the set of markers determined to be present in the test canid genome to a database comprising a plurality of canid population profiles, wherein each canid population profile comprises genotype information for the set of markers in the canid population, and* wherein the database of canid population profiles comprises between about five and about 500 canid population profiles*; and*

(*c*) *determining the contributions of canid populations to the test canid genome.*

13. [The method of claim **1**, wherein] *A method for determining the contributions of canid populations to a canid genome, comprising:*

(*a*) *genotyping a sample obtained from a test canid to determine the identity of one or both alleles present in the test canid genome for each of a set of markers, wherein the set of markers is indicative of the contributions of canid populations to the genome of the test canid;*

(*b*) *using a specifically programmed computer comprising an algorithm to compare the identity of one or both alleles for each of the set of markers determined to be present in the test canid genome to a database comprising a plurality of canid population profiles, wherein each canid population profile comprises genotype information for the set of markers in the canid population and* the database of canid populations profiles [comprise] *comprises* profiles for at least about five American Kennel Club registered breeds*; and*

(*c*) *determining the contributions of canid populations to the test canid genome.*

16. The method of claim [**1**] *13*, wherein step (a) comprises amplifying genomic DNA of the test canid using primers specific for each of the set of markers and determining the size of the amplification product.

17. The method of claim [**1**] *13*, wherein the algorithm according to step (b) comprises a genotype clustering program.

18. The method of claim [**1**] *13*, wherein the algorithm according to step (b) comprises an assignment algorithm.

19. The method of claim [**1**] *13*, wherein applying the algorithm according to step (b) comprises determining the probability that a specific canid population contributed to the genome of the test canid by determining the conditional probablility that the alleles in the test canid genome would occur in the specific canid population divided by the sum of conditional probabilities that the alleles in the test canid genome would occur in each canid population in the database.

20. The method of claim [**1**] *13*, wherein step (b) comprises discriminating between the contributions of two or more genetically related canid populations to the test canid genome by comparing the alleles in the test canid genome to a database comprising profiles of the two or more genetically related canid populations.

21. [The method of claim **20**] *A method for determining the contributions of canid populations to a canid genome, comprising:*

(*a*) *genotyping a sample obtained from a test canid to determine the identity of one or both alleles present in* *the test canid genome for each of a set of markers, wherein the set of markers is indicative of the contributions of canid populations to the genome of the test canid;*

(*b*) *using a specifically programmed computer comprising an algorithm to compare the identity of one or both alleles for each of the set of markers determined to be present in the test canid genome to a database comprising a plurality of canid population profiles, wherein each canid population profile comprises genotype information for the set of markers in the canid population, and wherein step* (*b*) *comprises discriminating between the contributions of two or more genetically related canid populations to the test canid genome by comparing the alleles in the test canid genome to a database comprising profiles of the two or more genetically related canid populations, and* wherein the two or more genetically related canid populations comprise Belgian Sheep Dog and Belgian Tervuren*; and*

(*c*) *determining the contributions of canid populations to the test canid genome.*

22. **[**The method of claim **20**,**]** *A method for determining the contributions of canid populations to a canid genome, comprising:*

(*a*) *genotyping a sample obtained from a test canid to determine the identity of one or both alleles present in the test canid genome for each of a set of markers, wherein the set of markers is indicative of the contributions of canid populations to the genome of the test canid;*

(*b*) *using a specifically programmed computer comprising an algorithm to compare the identity of one or both alleles for each of the set of markers determined to be present in the test canid genome to a database comprising a plurality of canid population profiles, wherein each canid population profile comprises genotype information for the set of markers in the canid population, and wherein step* (*b*) *comprises discriminating between the contributions of two or more genetically related canid populations to the test canid genome by comparing the alleles in the test canid genome to a database comprising profiles of the two or more genetically related canid populations, and* wherein the two or more genetically related canid populations comprise Collie and Shetland Sheep Dog*; and*

(*c*) *determining the contributions of canid populations to the test canid genome.*

23. **[**The method of claim **20**,**]** *A method for determining the contributions of canid populations to a canid genome, comprising:*

(*a*) *genotyping a sample obtained from a test canid to determine the identity of one or both alleles present in the test canid genome for each of a set of markers, wherein the set of markers is indicative of the contributions of canid populations to the genome of the test canid;*

(*b*) *using a specifically programmed computer comprising an algorithm to compare the identity of one or both alleles for each of the set of markers determined to be present in the test canid genome to a database comprising a plurality of canid population profiles, wherein each canid population profile comprises genotype information for the set of markers in the canid population, and wherein step* (*b*) *comprises discriminating between the contributions of two or more genetically related canid populations to the test canid genome by comparing the alleles in the test canid genome to a database comprising profiles of the two or more genetically related canid populatons, and* wherein the two or more genetically related canid populations comprise Whippet and Greyhound*; and*

(*c*) *determining the contributions of canid populations to the test canid genome.*

24. **[**The method of claim **20**,**]** *A method for determining the contributions of canid populations to a canid genome, comprising:*

(*a*) *genotyping a sample obtained from a test canid to determine the identity of one or both alleles present in the test canid genome for each of a set of markers, wherein the set of markers is indicative of the contributions of canid populations to the genome of the test canid;*

(*b*) *using a specifically programmed computer comprising an algorithm to compare the identity of one or both alleles for each of the set of markers determined to be present in the test canid genome to a database comprising a plurality of canid population profiles, wherein each canid population profile comprises genotype information for the set of markers in the canid population, and wherein step* (*b*) *comprises discriminating between the contributions of two or more genetically related canid populations to the test canid genome by comparing the alleles in the test canid genome to a database comprising profiles of the two or more genetically related canid populations, and* wherein the two or more genetically related canid populations comprise Siberian Husky and Alaskan Malamute*; and*

(*c*) *determining the contributions of canid populations to the test canid genome.*

25. **[**The method of claim **20**,**]** *A method for determining the contributions of canid populations to a canid genome, comprising:*

(*a*) *genotyping a sample obtained from a test canid to determine the identity of one or both alleles present in the test canid genome for each of a set of markers, wherein the set of markers is indicative of the contributions of canid populations to the genome of the test canid;*

(*b*) *using a specifically programmed computer comprising an algorithm to compare the identity of one or both alleles for each of the set of markers determined to be present in the test canid genome to a database comprising a plurality of canid population profiles, wherein each canid population profile comprises genotype information for the set of markers in the canid population, and wherein step* (*b*) *comprises discriminating between the contributions of two or more genetically related canid populations to the test canid genome by comparing the alleles in the test canid genome to a database comprising profiles of the two or more genetically related canid populations, and* wherein the two or more genetically related canid populations comprise Mastiff and Bullmastiff*; and*

(*c*) *determining the contributions of canid populations to the test canid genome.*

26. **[**The method of claim **20**,**]** *A method for determining the contributions of canid populations to a canid genome, comprising:*

(*a*) *genotyping a sample obtained from a test canid to determine the identity of one or both alleles present in the test canid genome for each of a set of markers, wherein the set of markers is indicative of the contributions of canid populations to the genome of the test canid;*

- (*b*) *using a specifically programmed computer comprising an algorithm to compare the identity of one or both alleles for each of the set of markers determined to be present in the test canid genome to a database comprising a plurality of canid population profiles, wherein each canid population profile comprises genotype information for the set of markers in the canid population, and wherein step* (*b*) *comprises discriminating between the contributions of two or more genetically related canid populations to the test canid genome by comparing the alleles in the test canid genome to a database comprising profiles of the two or more genetically related canid populations, and* wherein the two or more genetically related canid populations comprise Greater Swiss Mountain Dog and Bernese Mountain Dog*; and*
- (*c*) *determining the contributions of canid populations to the test canid genome.*

27. [The method of claim **20**,] *A method for determining the contributions of canid populations to a canid genome, comprising:*

- (*a*) *genotyping a sample obtained from a test canid to determine the identity of one or both alleles present in the test canid genome for each of a set of markers, wherein the set of markers is indicative of the contributions of canid populations to the genome of the test canid;*
- (*b*) *using a specifically programmed computer comprising an algorithm to compare the identity of one or both alleles for each of the set of markers determined to be present in the test canid genome to a database comprising a plurality of canid population profiles, wherein each canid population profile comprises genotype information for the set of markers in the canid population, and wherein step* (*b*) *comprises discriminating between the contributions of two or more genetically related canid populations to the test canid genome by comparing the alleles in the test canid genome to a database comprising profiles of the two or more genetically related canid populations, and* wherein the two or more genetically related canid populations comprise West Highland White Terrier and Cairn Terrier*; and*
- (*c*) *determining the contributions of canid populations to the test canid genome.*

28. [The method of claim **20**,] *A method for determining the contributions of canid populations to a canid genome, comprising:*

- (*a*) *genotyping a sample obtained from a test canid to determine the identity of one or both alleles present in the test canid genome for each of a set of markers, wherein the set of markers is indicative of the contributions of canid populations to the genome of the test canid;*
- (*b*) *using a specifically programmed computer comprising an algorithm to compare the identity of one or both alleles for each of the set of markers determined to be present in the test canid genome to a database comprising a plurality of canid population profiles, wherein each canid population profile comprises genotype information for the set of markers in the canid population, and wherein step* (*b*) *comprises discriminating between the contributions of two or more geneticfally related canid populations to the test canid genome by comparing the alleles in the test canid genome to a database comprising profiles of the two or more genetically related canid populations, and* wherein the two or more genetically related canid populations comprise Lhasa Apso, Shih Tzu, and Pekinese*; and*
- (*c*) *determining the contributions of canid populations to the test canid genome.*

31. [The method of claim **1**,] *A method for determining the contributions of canid populations to a canid genome, comprising:*

- (*a*) *genotyping a sample obtained from a test canid to determine the identity of one or both alleles present in the test canid genome for each of a set of markers, wherein the set of markers is indicative of the contributions of canid populations to the genome of the test canid;*
- (*b*) *using a specifically programmed computer comprising an algorithm to compare the identity of one or both alleles for each of the set of markers determined to be present in the test canid genome to a database comprising a plurality of canid population profiles, wherein each canid population profile comprises genotype information for the set of markers in the canid population; and*
- (*c*) *determining the contributions of canid populations to the test canid genome, and further providing a document displaying the contributions of one or more canid populations to the genome of the test canid genome, wherein the document provides additional information regarding the one or more canid populations that contributed to the genome of the test canid or the test canid and* wherein the additional information is health-related information.

33. [The method of claim **29**,] *A method for determining the contributions of canid populations to a canid genome, comprising:*

- (*a*) *genotyping a sample obtained from a test canid to determine the identity of one or both alleles present in the test canid genome for each of a set of markers, wherein the set of markers is indicative of the contributions of canid populations to the genome of the test canid;*
- (*b*) *using a specifically programmed computer comprising an algorithm to compare the identity of one or both alleles for each of the set of markers determined to be present in the test canid genome to a database comprising a plurality of canid population profiles, wherein each canid population profile comprises genotype information for the set of markers in the canid population; and*
- (*c*) *determining the contributions of canid populations to the test canid genome, and further providing a document displaying the contributions of one or more canid populations to the genome of the test canid genome,* wherein the document provides a certification of the contributions of one or more canid populations to the genome of the test canid genome.

34. [The method of claim **29**,] *A method for determining the contributions of canid populations to a canid genome, comprising:*

- (*a*) *genotyping a sample obtained from a test canid to determine the identity of one or both alleles present in the test canid genome for each of a set of markers, wherein the set of markers is indicative of the contributions of canid populations to the genome of the test canid;*
- (*b*) *using a specifically programmed computer comprising an algorithm to compare the identity of one or both*

alleles for each of the set of markers determined to be present in the test canid genome to a database comprising a plurality of canid population profiles, wherein each canid population profile comprises genotype information for the set of markers in the canid population; and

(*c*) *determining the contributions of canid populations to the test canid genome, and further providing a document displaying the contributions of one or more canid populations to the genome of the test canid genome,* wherein the document provides a representation of the one or more canid populations that contributed to the genome of the test canid.

35. A method for defining one or more canid populations, comprising:

(a) performing a genotyping assay on a set of canid genomes, to determine the identity of one or both alleles for each of a set of markers, wherein the set of markers is indicative of the contributions of canid populations to the genomes of each member of the set of canids; and (b) applying a computer-implemented statistical model to define one or more distinct canid populations, wherein one or more distinct canid populations are characterized by a set of allele frequencies for each marker in the set of markers *and the one or more distinct canid populations comprise at least about five American Kennel Club registered breeds*.

36. A computer readable medium comprising stored thereon:

(a) a datastructure thereon for use in distinguishing canid populations, the data structure comprising:
  (i) a marker field, which is capable of storing the name of a marker or of an allele of the marker; and
  (ii) a genotype information field, which is capable of storing genotype information for the marker in a canid population, wherein a record comprises an instantiation of the marker field and an instantiation of the genotype information field and a set of records represents a canid population profile; and

(b) computer-executable instructions for implementing a method for determining the contributions of canid populations to a canid genome, comprising:
  (i) obtaining the identity of one or both alleles in a test canid genome for each of a set of markers; and
  (ii) determining the contributions of canid populations to the test canid genome by comparing the alleles in the test canid genome to a database comprising canid population profiles, wherein each canid population profile comprises genotype information for the set of markers in the canid population *and wherein the database of canid population profiles comprises at least about five American Kennel Club registered breeds*.

37. A computer-readable medium comprising a data structure stored thereon for use in distinguishing canid populations, the data structure comprising:

(a) a marker field, which is capable of storing the name of a marker or of an allele of the marker; and

(b) a genotype information field, which is capable of storing genotype information for the marker in a canid population, wherein a record comprises an instantiation of the marker field and an instantiation of the genotype information field and a set of records represents a canid population profile, wherein the marker field comprises a set of markers indicative of the contributions of canid populations to the genome of a test canid *and wherein the canid populations comprise at least about five American Kennel Club registered breeds*.

39. A method for determining the contributions of canid populations to a canid genome, comprising performing a genotyping assay on a sample obtained from a test canid to determine the identity of one or both alleles present in the test canid genome for each of a set of markers, wherein the set of markers is indicative of the contribution of canid populations to the genome of the test canid *and wherein the canid populations comprise at least about five American Kennel Club registered breeds*.

45. The method of claim 13, wherein the set of markers comprises single nucleotide polymorphisms (SNPs).

46. The method of claim 13, wherein the set of markers comprises one or more population-specific markers.

47. The method of claim 46, wherein the one or more population-specific markers comprise one or more SNP markers.

48. The method of claim 13 further comprising the step of providing a document displaying the contributions of one or more canid populations to the genome of the test canid genome.

49. The method of claim 48, wherein the document provides additional information regarding the one or more canid populations that contributed to the genome of the test canid or the test canid.

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